


```
PF 08-OCT-1993; 93WO-US009636.
XX
XX 25-NOV-1992; 92US-00980518.
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX Birkenbach M, Kieff E;
XX WPI; 1994-200183/24.
XX DR N-PSDB; AA064125.
XX
XX DNA coding for Epstein Barr Virus induced (EBI) polypeptide(s) and
XX antibodies to EBV1, 2 and 3 - useful for detecting EBV by hybridisation
XX or by immunosassay.
XX
XX Claim 8; Page 54-56; 84pp; English.
XX
XX EBV infected B lymphocytes recapitulate features of antigen stimulation
XX in enlarging, increasing RNA synthesis, expressing activation antigens
XX and adhesion molecules, secreting Ig and proliferating. Unlike antigen
XX stimulated B lymphocytes, EBV infected B lymphocytes continue to
XX proliferate (in vitro) as immortalised lymphoblastoid cell lines. Because
XX of the similar effects of EBV and antigen, EBV induced genes are likely
XX to include mediators of antigen induced B lymphocyte growth or
XX differentiation. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 378 AA;
SQ
Query Match 100.0%; Score 1922; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.9e-206;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLQPKMSVVLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNFKAMF 60
DB 1 MDLQPKMSVVLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNFKAMF 60
QY 61 LPIWYSIIICFVGLGNGLVLTYYFKRLKMTDPTVLLNLAVDILFLTLTPMAYSAAK 120
DB 61 LPIWYSIIICFVGLGNGLVLTYYFKRLKMTDPTVLLNLAVDILFLTLTPMAYSAAK 120
QY 121 SWEGVHFCKLIPIAYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
DB 121 SWEGVHFCKLIPIAYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 121 SWEGVHFCKLIPIAYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
DB 121 SWEGVHFCKLIPIAYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSALIAVTLSTIPBLLYSDDLQSSSEQAMRCSLITEHVEAFITIOVAQVNIQFLVPLAMS 240
DB 181 GSALIAVTLSTIPBLLYSDDLQSSSEQAMRCSLITEHVEAFITIOVAQVNIQFLVPLAMS 240
QY 241 FCYVITITLLOARNFERNKAIKVIIVAVVFIYFQLPYNGVLAQTVANFNITSSCEL 300
DB 241 FCYVITITLLOARNFERNKAIKVIIVAVVFIYFQLPYNGVLAQTVANFNITSSCEL 300
QY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVKFRNDIFKLFKDLGCLSOEQLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVKFRNDIFKLFKDLGCLSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378
RESULT 2
AAWS3622
ID AAWS3622 standard; protein; 378 AA.
XX
XX AAWS3622;
XX
XX 09-JUL-1998 (first entry)
XX
XX Epstein Barr virus induced protein 1 (EBI-1).
XX
XX Assessing; monitoring; foetal development; placental development;
XX Epstein Barr virus; EBV; induced gene 1; EBI-1.
```

```
XX
XX Homo sapiens.
XX
XX US5744301-A.
XX
XX 28-APR-1998.
XX
XX 02-FEB-1995; 95US-00383750.
XX
XX 25-NOV-1992; 92US-00980518.
XX PR 30-NOV-1994; 94US-00352678.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Kieff E, Birkenbach M;
XX WPI; 1998-271060/24.
XX DR N-PSDB; AAV25490.
XX
XX Assessing or monitoring foetal or placental development - comprises
XX detecting the level or size of Epstein Barr virus induced nucleic acid or
XX protein in maternal serum samples.
XX
XX Example 2; Col 37-40; 45pp; English.
XX
XX The present sequence was used in the development of a novel method for
XX assessing or monitoring foetal or placental development. The method
XX comprises taking a maternal serum sample, and detecting the level or size
XX of Epstein Barr virus (EBV) induced gene or protein 3 (EBI-3) to obtain a
XX result, which can be compared to a control to assess or monitor foetal or
XX placental development
XX
XX Sequence 378 AA;
SQ
Query Match 100.0%; Score 1922; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.9e-206;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLQPKMSVVLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNFKAMF 60
DB 1 MDLQPKMSVVLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKQDVNFKAMF 60
QY 61 LPIWYSIIICFVGLGNGLVLTYYFKRLKMTDPTVLLNLAVDILFLTLTPMAYSAAK 120
DB 61 LPIWYSIIICFVGLGNGLVLTYYFKRLKMTDPTVLLNLAVDILFLTLTPMAYSAAK 120
QY 121 SWEGVHFCKLIPIAYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
DB 121 SWEGVHFCKLIPIAYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 121 SWEGVHFCKLIPIAYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
DB 121 SWEGVHFCKLIPIAYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSALIAVTLSTIPBLLYSDDLQSSSEQAMRCSLITEHVEAFITIOVAQVNIQFLVPLAMS 240
DB 181 GSALIAVTLSTIPBLLYSDDLQSSSEQAMRCSLITEHVEAFITIOVAQVNIQFLVPLAMS 240
QY 241 FCYVITITLLOARNFERNKAIKVIIVAVVFIYFQLPYNGVLAQTVANFNITSSCEL 300
DB 241 FCYVITITLLOARNFERNKAIKVIIVAVVFIYFQLPYNGVLAQTVANFNITSSCEL 300
QY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVKFRNDIFKLFKDLGCLSOEQLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVKFRNDIFKLFKDLGCLSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378
RESULT 3
AAWS6164
ID AAWS6164 standard; protein; 378 AA.
XX
XX AAWS6164;
XX
```

```

DT      20-JUL-1998 (first entry)
XX
XX      G-protein coupled receptor (R7G) designated EB11.
DE
XX      Lymphocyte R7G; EB11; G-protein coupled receptor;
XX      opiate/opioid recognition site; opiate; opioid; opioid binding protein;
XX      screening; lymphocyte receptor; compound; agonist; antagonist;
XX      lymphocyte receptor protein; immune-cell specific lymphocyte receptor;
XX      neuronal type opioid receptor.
XX
XX      Homo sapiens.
OS
XX      US5753516-A.
PN
XX      19-MAY-1998.
PD
XX      03-FEB-1995; 95US-00383751.
PF
XX      03-FEB-1995; 95US-00383751.
PR
XX      03-FEB-1995; 95US-00383751.
PA      (FINB/) FINBERG R W.
XX      (HEAG/) HEAGY W E.
PI
XX      Heagy WE, Finberg RW;
XX
XX      WPI: 1998-311410/27.
DR      N-PSDB; AAV22684.
XX
XX      Screening assay for lymphocyte opioid receptor ligands - using
XX      recombinant receptor protein.
XX
XX      Claim 1; Col 87-88; 70pp; English.
XX
XX      The present sequence represents a novel lymphocyte R7G, termed EB11. R7G
XX      proteins are part of the G-protein coupled receptor superfamily. EB11 is
XX      a functional opiate/opioid recognition site that probably plays a major
XX      role in mediating the effects that opiate/opioids have on lymphocytes.
XX      The EB11 protein is an opioid binding protein that is displayed on the
XX      surface of lymphocytes. A process for screening a candidate substance for
XX      ability to interact with a lymphocyte receptor comprises selecting a
XX      candidate substance having a chemical structure or biological activity
XX      suggestive of an ability to mimic the biological activity of an opiate,
XX      opioid drug or opioid peptide having known binding affinity for EB11. The
XX      ability of the candidate substance is tested to interact with the
XX      lymphocyte receptor protein. This method can be used to screen for
XX      agonists or antagonists to the lymphocyte receptor protein. The method
XX      can be modified and used to screen for agonists or antagonists to the
XX      immune-cell specific lymphocyte receptor polypeptide or the neuronal type
XX      opioid receptor polypeptide
XX
XX      Sequence 378 AA;
XX
XX
XX      Query Match      100.0%; Score 1922; DB 2; Length 378;
XX      Best Local Similarity 100.0%; Pred. No. 1.9e-206;
XX      Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX      1 MDLGRKMSVSLVALLVIFQVCLACDEVTDDYIGNTTVDYTLFESLCSKKDVRNFKAMF 60
XX      1 MDLGRKMSVSLVALLVIFQVCLACDEVTDDYIGNTTVDYTLFESLCSKKDVRNFKAMF 60
XX
XX      61 LPIMYSIIICPGGLGNGLVLTYYIFKRLKMTDTYLLNLAVADILFLITTFMAYSAK 120
XX      61 LPIMYSIIICPGGLGNGLVLTYYIFKRLKMTDTYLLNLAVADILFLITTFMAYSAK 120
XX
XX      121 SWEVGVHCKLIFALYKMSFSGMILLICISIDRYVAIVQASARHRRARVLLISKGV 180
XX      121 SWEVGVHCKLIFALYKMSFSGMILLICISIDRYVAIVQASARHRRARVLLISKGV 180
XX
XX      181 GSAILATVLSIPELLYSDLRSSSSQARCSLITEHVEAFITQVAQWYIGLVPLAMS 240
XX      181 GSAILATVLSIPELLYSDLRSSSSQARCSLITEHVEAFITQVAQWYIGLVPLAMS 240
XX
XX      241 FGYLVIITTLQARNFERNKAIKVIAVVVFIVEQLPYNGVLAQTVAENFITSSTCEL 300
XX      241 FGYLVIITTLQARNFERNKAIKVIAVVVFIVEQLPYNGVLAQTVAENFITSSTCEL 300

```

Db	241	FCVLVIIRTLQABNERKAKIIVAVVPIVQGLPYNGVLAQIVYANNTISSICEL	3000
Qy	301	SKQLNIAVDVTVSLACVRCVNPFLYAFIGVFXENDIFKLFKDIAGCLSQEQLRQWSSCRH	3600
Db	301	SKQLNIAVDVTVSLACVRCVNPFLYAFIGVFXENDIFKLFKDIAGCLSQEQLRQWSSCRH	3600
Qy	361	IRRSSMSVEAETTTTFFSP 378	
Db	361	IRRSSMSVEAETTTTFFSP 378	
RESULT 4			
ADNR03499	ADR03499	standard; protein, 378 AA.	
XX	XX	ADR03499;	
XX	XX	21-OCT-2004 (first entry)	
XX	XX	Cytokine receptor CCR7.	
XX	XX	antiallergic; antiinflammatory; antimicrobial; cytostatic;	
XX	XX	immunostimulant; immunosuppressive; CCX chemokine receptor; CCX CR;	
XX	XX	EB11-ligand chemokine; ELC; secondary lymphoid-tissue chemokine; SLC;	
XX	XX	thymus-expressed chemokine; TECK; chemokine binding activity;	
XX	XX	CCR CR modulator; chemokine binding modulator; inflammation; allergy;	
XX	XX	autoimmune disease; graft rejection; cancer; infectious disease;	
XX	XX	immunosuppressive disease; CCR7.	
XX	XX	Unidentified.	
XX	XX	US2004146926-A1.	
XX	XX	29-JUL-2004.	
XX	XX	24-FEB-2004; 2004US-00787018.	
XX	XX	12-OCT-1999; 99US-0159015P.	
XX	XX	13-OCT-1999; 99US-0159210P.	
XX	XX	20-DEC-1999; 99US-0172979P.	
XX	XX	28-DEC-1999; 99US-0173388P.	
XX	XX	03-MAR-2000; 2000US-0186626P.	
XX	XX	10-OCT-2000; 2000US-00686019.	
XX	XX	21-NOV-2000; 2000US-00721495.	
XX	XX	(CHEM-) CHEMOCENTRXX INC.	
XX	XX	Geisling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;	
XX	XX	WPI; 2004-5613394/54.	
XX	XX	New CCX chemokine receptor polypeptide that binds ELC, SLC or TECK,	
XX	XX	useful in identifying modulators of its expression or activity which are	
XX	XX	potentially useful for treating inflammation, allergies, autoimmune	
XX	XX	disease and cancer.	
XX	XX	Example 1; Fig 2A; 37pp; English.	
XX	XX	The invention describes an isolated or recombinant CCX chemokine receptor	
XX	XX	(CCX CR) polypeptide (1) or its fragment that binds EB11-ligand	
XX	XX	chemokine (ELC), secondary lymphoid-tissue chemokine (SLC) or thymus-	
XX	XX	expressed chemokine (TECK). Also described are: a fusion protein	
XX	XX	comprising the polypeptide; an isolated polynucleotide encoding (1) or	
XX	XX	its fragment; an isolated polynucleotide comprising a sequence encoding a	
XX	XX	polypeptide that has a chemokine binding activity which is: a	
XX	XX	polynucleotide comprising the sequence of SEQ ID NO:1 or SEQ ID NO:3; a	
XX	XX	polynucleotide that hybridises under stringent conditions to (a); or a	
XX	XX	polynucleotide sequence which is degenerate as a result of the genetic	
XX	XX	code to the sequences defined in (a) or (b); a recombinant (expression)	
XX	XX	vector comprising the polynucleotide; a host cell comprising the vector;	
XX	XX	producing a CCX CR protein, peptide or fusion protein; a polynucleotide	
XX	XX	primer, probe, antisense oligonucleotide or ribozyme comprising at least	

CC 15 contiguous bases identical or exactly complementary to the 1147-bp
CC sequence; an antibody or its fragment that specifically binds to the
CC polypeptide; an isolated cell capable of secreting the antibody; a
CC hybridoma capable of secreting the antibody; detecting a CCX CKR gene
CC product in a sample; amplifying a CCX CKR polynucleotide in a sample;
CC identifying a modulator of the binding of CCX CKR to a chemokine;
CC producing a pharmaceutical composition from a modulator of CCX CKR
CC (chemokine binding) activity; identifying a modulator of CCX CKR activity
CC and treating a CCX CKR-mediated condition in a mammal. Agents that
CC modulate the activity of CCX CKR in a cell or tissue in an animal are
CC useful for treating CCX CKR related conditions such as inflammation,
CC allergy, an autoimmune disease, graft rejection, cancer, an infectious
CC disease or an immunosuppressive disease, preferably inflammation. This is
CC the amino acid sequence of a cytokine receptor CCR7, used in a comparison
CC with human cytokine receptor CCX CKR of the invention.

XX Sequence 378 AA;

Query Match 100.0%; Score 1922; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.9e-206;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAMF 60
QY 61 LPIWYSIIICFVGLGNGLVLTYYIFKRLKMTDTYLLNLAVADILFLTLTPFMAYSAAK 120
DB 61 LPIWYSIIICFVGLGNGLVLTYYIFKRLKMTDTYLLNLAVADILFLTLTPFMAYSAAK 120
QY 121 SWFGVHFCKLIIFAIYKMSFFSGMLLLICISIDRVVAIVQAVSARHRRARVLLISKSCV 180
DB 121 SWFGVHFCKLIIFAIYKMSFFSGMLLLICISIDRVVAIVQAVSARHRRARVLLISKSCV 180
QY 181 GSALIAATVLSIPELLYSLORSSSEQARCSLITHEHVAFTTIOVAQWVIGFVLPLAMS 240
DB 181 GSALIAATVLSIPELLYSLORSSSEQARCSLITHEHVAFTTIOVAQWVIGFVLPLAMS 240
QY 241 FCYLVIIKTLQARNFERKAIKVIIVAVVFIQOLPYNGVLAQTVANFNITSSTCEL 300
DB 241 FCYLVIIKTLQARNFERKAIKVIIVAVVFIQOLPYNGVLAQTVANFNITSSTCEL 300
QY 301 SKQINIAVDVTSIACVRCVNPFLYAFIGVFRNDIFKLPKDLGCLSOEQLRQWSSCRH 360
DB 301 SKQINIAVDVTSIACVRCVNPFLYAFIGVFRNDIFKLPKDLGCLSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378

RESULT 5
AAW48724
ID AAW48724 standard; protein; 378 AA.

XX AAW48724;

DT 25-SEP-1998 (first entry)

XX Human V31 seven transmembrane receptor.

XX V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
KW immunology; inflammation; V31.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 58..86

FT Domain /note= "Transmembrane domain 1"

FT Domain 96..119

FT Domain /note= "Transmembrane domain 2"

FT Domain 131..152

FT Domain /note= "Transmembrane domain 3"

FT Domain 171..196
FT /note= "Transmembrane domain 4"
FT Domain 219..247
FT /note= "Transmembrane domain 5"
FT Domain 264..285
FT /note= "Transmembrane domain 6"
FT Domain 306..331
FT /note= "Transmembrane domain 7"

PN US5759804-A.

PD 02-JUN-1998.

XX 17-NOV-1993; 93US-00153848.

XX 17-NOV-1992; 92US-00977452.

XX (ICOS-) ICOS CORP.

XX Schwickart VL, Godiska R, Gray PW;

XX WPI, 1998-332132/29.

XX N-PSDB; AAV18347.

PT DNA encoding V28 seven transmembrane receptor polypeptide - useful for
PT producing recombinant polypeptide and anti-V28 antibodies, and in
PT screening assays for V28 agonists and antagonists.

PS Example 3; Col 39-42; 56pp; English.

CC The present sequence represents the V31 seven transmembrane (7TM)
CC receptor encoded by the V31 cDNA (AAV18347). The invention claims for a
CC full length V28 genomic DNA (AAV18343) and the V28 protein it encodes
CC (AAW48722). V28 and V31 proteins are 7TM receptors which are probably
CC involved in signal transduction. The invention also claims that cells
CC transformed with V28 DNA can be used to produce the recombinant
CC polypeptide, to produce anti-V28 antibodies or in screening assays for
CC V28 agonists or antagonists. The antibodies, agonists and antagonists
CC could then be used to modulate V28 receptor-ligand binding, for e.g. in
CC immunological and/or inflammatory events in vivo

SQ Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 2; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFESLCSKKDVRNFKAMF 60
QY 61 LPIWYSIIICFVGLGNGLVLTYYIFKRLKMTDTYLLNLAVADILFLTLTPFMAYSAAK 120
DB 61 LPIWYSIIICFVGLGNGLVLTYYIFKRLKMTDTYLLNLAVADILFLTLTPFMAYSAAK 120
QY 121 SWFGVHFCKLIIFAIYKMSFFSGMLLLICISIDRVVAIVQAVSARHRRARVLLISKSCV 180
DB 121 SWFGVHFCKLIIFAIYKMSFFSGMLLLICISIDRVVAIVQAVSARHRRARVLLISKSCV 180
QY 181 GSALIAATVLSIPELLYSLORSSSEQARCSLITHEHVAFTTIOVAQWVIGFVLPLAMS 240
DB 181 GSALIAATVLSIPELLYSLORSSSEQARCSLITHEHVAFTTIOVAQWVIGFVLPLAMS 240
QY 241 FCYLVIIKTLQARNFERKAIKVIIVAVVFIQOLPYNGVLAQTVANFNITSSTCEL 300
DB 241 FCYLVIIKTLQARNFERKAIKVIIVAVVFIQOLPYNGVLAQTVANFNITSSTCEL 300
QY 301 SKQINIAVDVTSIACVRCVNPFLYAFIGVFRNDIFKLPKDLGCLSOEQLRQWSSCRH 360
DB 301 SKQINIAVDVTSIACVRCVNPFLYAFIGVFRNDIFKLPKDLGCLSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378

DB 361 IRRSSMSVEAETTTTSP 378

RESULT 6
AAB21688
ID AAB21688 standard; protein; 378 AA.
XX
AC AAB21688;
XX
DT 26-JAN-2001 (first entry)
XX
DE Human 7TM receptor V31-B cDNA clone protein.
XX
KW Seven transmembrane receptor; 7TM; heptahelical; serpentine;
KW G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
KW cancer.
XX
OS Homo sapiens.
XX
PN US6107475-A.
XX
PD 22-AUG-2000.
XX
PF 26-APR-1999; 99US-00299843.
XX
PR 17-NOV-1992; 92US-00977452.
PR 17-NOV-1993; 93US-00153848.
PR 17-MAY-1994; 94US-00245242.
PR 01-JUN-1998; 98US-00088337.
XX
PA (ICOS-) ICOS CORP.
XX
PI Schwellkart VL, Gray PW, Godiska R;
XX
DR WPI, 2000-571335/53.
DR N-PSDB; AAA91707.
XX
PT Polynucleotide encoding seven transmembrane receptors, antibody specific
PT to the receptor, agonist and antagonist of the receptor useful for
PT treating inflammation in a mammal.
XX
PS Example 3; Col 41-44; 61pp; English.
XX
CC The present sequence is a novel seven transmembrane (7TM) receptors (also
CC known as heptahelical, serpentine or G-protein-coupled receptors). The
CC coding sequence for the present sequence may be used for gene therapy for
CC diseases such as cancer
XX
SQ Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 3; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVVALVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKQDVNRKAMF 60
DB 1 MDLGRKMSVLLVVALVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKQDVNRKAMF 60
QY 61 LPIWMSIIFPVGLGNGLVLLTYIYRKLKMTDTYTLANAVDILFLTLPPWASAAK 120
DB 61 LPIWMSIIFPVGLGNGLVLLTYIYRKLKMTDTYTLANAVDILFLTLPPWASAAK 120
QY 121 SWVFGVHFCKLIPAIYKMSFPGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
DB 121 SWVFGVHFCKLIPAIYKMSFPGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
QY 181 GSAILATVLSIDELYSIDLRSSSEQAMRCSLITEHVEAFITIQVAMVIGFLVPLLAWS 240
DB 181 GSAILATVLSIDELYSIDLRSSSEQAMRCSLITEHVEAFITIQVAMVIGFLVPLLAWS 240
QY 241 FCYLVIRTLQARNERNKAIYVIAVVVFVFPOLPNGVLLAQTAVANFNITSTCEI 300
DB 241 FCYLVIRTLQARNERNKAIYVIAVVVFVFPOLPNGVLLAQTAVANFNITSTCEI 300

QY 301 SKOLNIADVTVSLACVRCVNPFLYAFIGVFRNDIFKLFQDGLSQEQLRQWSSCRH 360
DB 301 SKOLNIADVTVSLACVRCVNPFLYAFIGVFRNDIFKLFQDGLSQEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378

RESULT 7
AAG80114
ID AAG80114 standard; protein; 378 AA.
XX
AC AAG80114;
XX
DT 17-JAN-2002 (first entry)
XX
DE Human CCR7 protein.
XX
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiaschmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP003708.
XX
PR 31-MAR-2000; 2000DE-01016013.
XX
PA (IPFP-) IFF PHARM GMBH.
PA (FORS/) FORSMANN U.
XX
PI Forsemann W, Adermann K, Heitland A, Spodeberg N;
XX
DR WPI, 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands, useful
PT for detecting tumors, inflammation etc., also therapeutic use of ligand
PT inhibitors.
XX
PS Disclosure; Page 10; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiaschmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention
XX
SQ Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 4; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVVALVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKQDVNRKAMF 60

```

Db      1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTVDTYTLFSLCSKKQVRNFKAMF 60
Qy      61 LPIMYSIICFVGLGNGVLVLTYYIFKRLKMTDYYLNLAVADILFLLTFPMAYSAK 120
Db      61 LPIMYSIICFVGLGNGVLVLTYYIFKRLKMTDYYLNLAVADILFLLTFPMAYSAK 120
Qy      121 SWFGVHFCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db      121 SWFGVHFCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Qy      181 GSAILATVLSIPELLYSDLRSSSEQAMRCSLITEHVEAFITIQVQAVIGFVPLLAMS 240
Db      181 GIWILATVLSIPELLYSDLRSSSEQAMRCSLITEHVEAFITIQVQAVIGFVPLLAMS 240
Qy      241 FCYLVITIRTLQARNFERNKAIKVLIIVVVFIVQLPYNGVLAQTVAENFITSSTCEL 300
Db      241 FCYLVITIRTLQARNFERNKAIKVLIIVVVFIVQLPYNGVLAQTVAENFITSSTCEL 300
Qy      301 SKQNLAIADVTYSLACVRCVNPFLYAFIYGVKFRNDIFKLFDLGLCSOEQLRQMSGRH 360
Db      301 SKQNLAIADVTYSLACVRCVNPFLYAFIYGVKFRNDIFKLFDLGLCSOEQLRQMSGRH 360
Qy      361 IRRSSMSVEAETTTTFSP 378
Db      361 IRRSSMSVEAETTTTFSP 378

```

RESULT 8
AAB50859
ID AAB50859 standard; protein, 378 AA.

AC AAB50859;
DT 16-MAR-2001 (first entry)
DE Human CCR7.

Human; chemokine receptor 7; CCR7; chemokine beta-9; Ckbeta-9; allergy;
autoimmune disease; ischaemia; atherosclerosis; cancer;
chronic inflammatory disorder; organ transplant; tissue graft;
chronic myelogenous leukaemia; infection.

OS Homo sapiens.

PN US6153441-A.

PD 28-NOV-2000.

PF 17-FEB-1999; 99US-00251545.

PR 17-FEB-1998; 98US-0074883P.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI Appelbaum ER, White JR, Sarau HM;

DR WPI; 2001-049151/06.

Identifying agonists or antagonists of interaction between human protein,
chemokine beta-9 and human CC chemokine receptor 7, by contacting cell
expressing receptor with test compound.

Claim 1; Fig 1; 20pp; English.

The present sequence is human chemokine receptor 7 (CCR7), a cellular
receptor for chemokine beta-9 (Ckbeta-9). The sequence may be used in a
method for discovering agonists and antagonists of the interaction
between Ckbeta-9 and CCR7. A cell expressing CCR7 polypeptide on its
surface, associated with a component capable of providing a detectable
signal in response to binding of Ckbeta-9, is contacted with a compound
in the presence of labelled or unlabelled Ckbeta-9. The compound is
identified as an agonist/antagonist by determining whether it activates

or inhibits the detectable signal. The method is useful for identifying
agonists and antagonists of the interaction between Ckbeta-9 and CCR7
which are useful for treating diseases including allergic disorders,
autoimmune diseases, ischaemia/reperfusion injury, development of
atherosclerotic plaques, cancer, chronic inflammatory disorders, chronic
rejection of transplanted organs or tissue grafts, chronic myelogenous
leukaemia, and infection by HIV and other pathogens

Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 4; Length 378;
Best Local Similarity 99.2%; Pred. No. 9, 1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTVDTYTLFSLCSKKQVRNFKAMF 60
Db      1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTVDTYTLFSLCSKKQVRNFKAMF 60
Qy      61 LPIMYSIICFVGLGNGVLVLTYYIFKRLKMTDYYLNLAVADILFLLTFPMAYSAK 120
Db      61 LPIMYSIICFVGLGNGVLVLTYYIFKRLKMTDYYLNLAVADILFLLTFPMAYSAK 120
Qy      121 SWFGVHFCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db      121 SWFGVHFCKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Qy      181 GSAILATVLSIPELLYSDLRSSSEQAMRCSLITEHVEAFITIQVQAVIGFVPLLAMS 240
Db      181 GIWILATVLSIPELLYSDLRSSSEQAMRCSLITEHVEAFITIQVQAVIGFVPLLAMS 240
Qy      241 FCYLVITIRTLQARNFERNKAIKVLIIVVVFIVQLPYNGVLAQTVAENFITSSTCEL 300
Db      241 FCYLVITIRTLQARNFERNKAIKVLIIVVVFIVQLPYNGVLAQTVAENFITSSTCEL 300
Qy      301 SKQNLAIADVTYSLACVRCVNPFLYAFIYGVKFRNDIFKLFDLGLCSOEQLRQMSGRH 360
Db      301 SKQNLAIADVTYSLACVRCVNPFLYAFIYGVKFRNDIFKLFDLGLCSOEQLRQMSGRH 360
Qy      361 IRRSSMSVEAETTTTFSP 378
Db      361 IRRSSMSVEAETTTTFSP 378

```

RESULT 9

AAU91230
ID AAU91230 standard; protein, 378 AA.

AC AAU91230;

DT 18-JUN-2002 (first entry)

DE Human 7 transmembrane domain receptor V31 #2.

Human; 7 transmembrane domain receptor; 7TM; antiinflammatory;
immunomodulatory; immunological disease; inflammation;
familial breast cancer; von Hippel-Lindau syndrome;
thyroid hormone resistance; small cell cancer of the lung;
pseudo-Zellweger syndrome; hypoprolthrombinaemia; dysprothrombinaemia.

OS Homo sapiens.

PN US6348574-B1.

PD 19-FEB-2002.

PF 01-JUN-1998; 98US-00088337.

PR 17-NOV-1992; 92US-00977452.

PR 17-NOV-1993; 93US-00153848.

PR 17-MAY-1994; 94US-00245242.

PA (ICOS-) ICOS CORP.

Identified as an agonist/antagonist by determining whether it activates

PI Godiska R, Gray PW, Schweickart VL;

XX WPI; 2002-266543/31.
DR N-PSDB; ABK54236.

XX New seven transmembrane receptor polypeptide R2, useful for producing
PT antibodies capable of modulating ligand/receptor binding reactions
PT involved in in vivo immunological and/or inflammatory events.

PS Example 3; Col 41-44; 61pp; English.

XX The invention relates to a purified and isolated R2 seven transmembrane
CC (7TM) receptor. Also included are an anti-R2 antibody, a hybridoma
CC producing the antibody, antigenic peptide fragments of R2, an antiserum
CC produced by immunising a mammal with a composition comprising R2 or its
CC fragment, where the fragment comprises at least one R2 extracellular or
CC intracellular domain, and obtaining antiserum from the mammal after the
CC immunising step, where the antiserum contains antibodies that bind to the
CC R2 7TM receptor, a polynucleotide encoding 7TM receptor R2 and a host
CC cell stably transformed or transfected with the polynucleotide allowing
CC the expression of R2 in the host cell. The antibody is useful for
CC modulating ligand/antigen binding of a R2 7TM receptor, especially
CC those ligand/receptor binding reactions involved in immunological and/or
CC inflammatory events in vivo. R2 is useful for producing antibodies. The
CC antibody is useful for immunisation to generate anti-idiotypic
CC antibodies, for purifying R2 polypeptides, for identifying cells
CC producing the polypeptides on their surfaces and for the detection and
CC quantification of 7TM receptors on cell surfaces and in fluids. The
CC polynucleotide is useful in DNA/RNA hybridisation assays to detect the
CC capacity of cells to synthesise a 7TM receptor. The host cell is useful
CC for large scale production of 7TM receptors, and in assays for
CC identifying antagonist or agonists of 7TM receptor binding. Other 7TM
CC receptors isolated in this study include V31 (located on chromosome 17q12
CC -21.2, associated with familial breast cancer), V28 (chromosome 3p21-ter,
CC associated with von Hippel-Lindau syndrome, thyroid hormone resistance,
CC small cell cancer of the lung and pseudo-Zellweger syndrome), R20
CC (chromosome 11 p11-p13 associated with hypoproteinaemia and
CC dysproteinaemia), V112 and R12. The present sequence is a 7TM
CC receptor of the invention

XX Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 5; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMF 60
OY 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMF 60
DB 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMF 60
OY 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMF 60
DB 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYTLNLAVADILFLLTLPFMAYSAK 120
OY 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYTLNLAVADILFLLTLPFMAYSAK 120
DB 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYTLNLAVADILFLLTLPFMAYSAK 120
OY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
OY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
OY 181 GSAILATVLSIPBLLYSDLRSSSSQAMKCSLITHEVEAFITIOVAOMVIGLVPPLAMS 240
DB 181 GSAILATVLSIPBLLYSDLRSSSSQAMKCSLITHEVEAFITIOVAOMVIGLVPPLAMS 240
OY 181 GSAILATVLSIPBLLYSDLRSSSSQAMKCSLITHEVEAFITIOVAOMVIGLVPPLAMS 240
DB 181 GSAILATVLSIPBLLYSDLRSSSSQAMKCSLITHEVEAFITIOVAOMVIGLVPPLAMS 240
OY 241 FCYLVITRTLOARNFERKAIKVIIVAVVPIVQPLPNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVITRTLOARNFERKAIKVIIVAVVPIVQPLPNGVLAQTVANFNITSTCEL 300
OY 241 FCYLVITRTLOARNFERKAIKVIIVAVVPIVQPLPNGVLAQTVANFNITSTCEL 300
DB 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDLFLKFDLGLSGEQRLQWSSCGH 360
OY 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDLFLKFDLGLSGEQRLQWSSCGH 360
DB 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDLFLKFDLGLSGEQRLQWSSCGH 360
OY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378

RESULT 10
ABP97730
ID ABP97730 standard; protein; 378 AA.

XX ABP97730;
AC ABP97730;
XX 28-MAY-2003 (first entry)

DE Amino acid sequence of human chemokine receptor CCR7.

XX Human; chemokine receptor; CCR7; viral infection; surface protein;
XX respiratory virus infection; respiratory syncytial virus infection;
XX RSV infection; bronchiolitis; bronchitis; pneumonia; asthma.

OS Homo sapiens.

XX WO2003014153-A2.

XX 20-FEB-2003.

XX 12-AUG-2002; 2002WO-CA001248.

XX 10-AUG-2001; 2001US-0311088P.

XX (TOP1-) TOPIGEN PHARM INC.

XX Renzi P, Zemzouni K;

XX WPI; 2003-256541/25.

DR N-PSDB; ABK68883.

PT Modulating viral infection of a cell, for treating or preventing
PT respiratory virus infections, bronchitis, pneumonia or asthma, by
PT modulating a binding interaction between a cell chemokine-receptor and a
PT surface protein of the virus.

PS Disclosure; Page 106-107; 120pp; English.

XX The present sequence represents human chemokine receptor CCR7. The
CC specification describes a method for modulating viral infection of a
CC cell. The method comprises modulating a binding interaction between a
CC cell chemokine-receptor and a surface protein of the virus. The proviso
CC is that the cell chemokine-receptor is not CX3CR1 and that the virus is
CC not HIV. The method is useful for treating or preventing respiratory
CC virus infection in vertebrates, more particularly respiratory syncytial
CC virus (RSV) infections, and related diseases, e.g. bronchiolitis,
CC bronchitis, pneumonia or asthma

XX Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 6; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMF 60
DB 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMF 60
OY 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMF 60
DB 1 MDLGRPMKSVLVALLVIFQVCLCODEVTDYIGNTTYDYLTFESLCKKQVRNFKAMF 60
OY 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYTLNLAVADILFLLTLPFMAYSAK 120
DB 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYTLNLAVADILFLLTLPFMAYSAK 120
OY 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYTLNLAVADILFLLTLPFMAYSAK 120
DB 61 LPIMTSIICFVGLNGVLVLTYYIFPKRLKMTDTYTLNLAVADILFLLTLPFMAYSAK 120
OY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
OY 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
OY 181 GSAILATVLSIPBLLYSDLRSSSSQAMKCSLITHEVEAFITIOVAOMVIGLVPPLAMS 240
DB 181 GSAILATVLSIPBLLYSDLRSSSSQAMKCSLITHEVEAFITIOVAOMVIGLVPPLAMS 240
OY 181 GSAILATVLSIPBLLYSDLRSSSSQAMKCSLITHEVEAFITIOVAOMVIGLVPPLAMS 240
DB 181 GSAILATVLSIPBLLYSDLRSSSSQAMKCSLITHEVEAFITIOVAOMVIGLVPPLAMS 240
OY 241 FCYLVITRTLOARNFERKAIKVIIVAVVPIVQPLPNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVITRTLOARNFERKAIKVIIVAVVPIVQPLPNGVLAQTVANFNITSTCEL 300

Db 241 FCYLVITITLLQANRFRNKAIKVIIAVWVFIVFQLPYNGVLAQTANFNITSTCEL 300
 QY 301 SKQINIAVDVTVSLACVACCNPFLLYAFIVGVKFRNDIFKLFRDGLCSOEQLRQWSSCRH 360
 Db 301 SKQINIAVDVTVSLACVACCNPFLLYAFIVGVKFRNDIFKLFRDGLCSOEQLRQWSSCRH 360
 QY 361 IRRSSMSVEAEETTTTFFSP 378
 Db 361 IRRSSMSVEAEETTTTFFSP 378
 RESULT 11
 ABP81793
 ID ABP81793 standard; protein, 378 AA.
 AC ABP81793;
 DT 04-MAR-2003 (first entry)
 DE Human C-C chemokine receptor 7 protein SEQ ID NO:68.
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX Homo sapiens.
 XX OS
 XX MO200261087-A2.
 XX PN 08-AUG-2002.
 XX PD 19-DEC-2001; 2001MO-US050107.
 XX PF 19-DEC-2000; 2000US-0257144P.
 XX PR 19-DEC-2000; 2000US-0257144P.
 XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX PI Burner GC, Roush CL, Brown JP;
 XX WPI; 2003-046718/04.
 XX DR N-PSDB; AB242637.
 XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX Disclousure; Fig 1; 523pp; English.
 PS The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,

CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242669 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX Sequence 378 AA:
 SQ
 Query Match 99.2%; Score 1907; DB 6; Length 378;
 Best Local Similarity 99.2%; Pred. No. 9.1e-205;
 Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MDLQKPMKSVLVALLVIFQVCLCODEVTDDYIGDNTVDYTLFESLCKKQDVRFKAMF 60
 Db 1 MDLQKPMKSVLVALLVIFQVCLCODEVTDDYIGDNTVDYTLFESLCKKQDVRFKAMF 60
 QY 61 LPIMYSIICFVGLGNGLVVLTYYFKRLKTMPTDYLLNLAVADILFLLTLPFMAVSAK 120
 Db 61 LPIMYSIICFVGLGNGLVVLTYYFKRLKTMPTDYLLNLAVADILFLLTLPFMAVSAK 120
 QY 121 SWFVGWFKLIPAIYKMSFFSGMLLCLISIDRYVAIVQAVSAHRHARVLLISKSCV 180
 Db 121 SWFVGWFKLIPAIYKMSFFSGMLLCLISIDRYVAIVQAVSAHRHARVLLISKSCV 180
 QY 181 GSALIAATLSIPELLVSPDLSRSSSEQAMRCSLIEHVEAFITIOVAQWVIGFLVPLAMS 240
 Db 181 GIWIAIATVLSIPELLVSPDLSRSSSEQAMRCSLIEHVEAFITIOVAQWVIGFLVPLAMS 240
 QY 241 FCYLVITITLLQANRFRNKAIKVIIAVWVFIVFQLPYNGVLAQTANFNITSTCEL 300
 Db 241 FCYLVITITLLQANRFRNKAIKVIIAVWVFIVFQLPYNGVLAQTANFNITSTCEL 300
 QY 301 SKQINIAVDVTVSLACVACCNPFLLYAFIVGVKFRNDIFKLFRDGLCSOEQLRQWSSCRH 360
 Db 301 SKQINIAVDVTVSLACVACCNPFLLYAFIVGVKFRNDIFKLFRDGLCSOEQLRQWSSCRH 360
 QY 361 IRRSSMSVEAEETTTTFFSP 378
 Db 361 IRRSSMSVEAEETTTTFFSP 378
 RESULT 12
 ADC22593
 ID ADC22593 standard; protein, 378 AA.
 AC ADC22593;
 DT 18-DEC-2003 (first entry)
 DE Human G protein-coupled receptor (GPCR) polypeptide #21.
 KW Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
 KW intracellular-3 region; IC3; receptor.
 XX Homo sapiens.
 XX OS
 XX US6555339-B1.
 XX PN 29-APR-2003.
 XX PD 13-OCT-1998; 98US-00170496.
 XX PF 14-APR-1997; 97US-00839449.
 XX PR 14-APR-1998; 98US-00060188.
 XX PR 26-JUN-1998; 98US-0090783P.
 XX PR 07-AUG-1998; 98US-0095677P.
 XX PA (AREN-) ARENA PHARM INC.

XX L1aw CW, Behan DP, Chalmers DT;
PI MPI; 2003-742861/70.
DR N-PSDB; ADC22592.
XX
PT Creating a constitutively active version of an endogenous human G protein
PT coupled receptor (GPCR) comprises substituting a specific amino acid in
PT the transmembrane-6 region with a different amino acid, and testing for
PT constitutive activity.
XX
PS Example 1; SEQ ID NO 74; 221bp; English.
XX
CC The invention relates to a method for creating a non-endogenous,
CC constitutively active version of an endogenous human G protein-coupled
CC receptor (GPCR) that has a transmembrane-6 (TM6) region and an
CC intracellular-3 (IC3) region, by substituting a specific amino acid in
CC the TM6 region with a different amino acid, and testing for constitutive
CC activity. The method is useful for creating a constitutively active
CC version of an endogenous human GPCR that comprises a transmembrane 6
CC region and an intracellular loop 3 region. The altered human GPCR
CC polypeptides are useful for screening test compounds for identification
CC of inverse agonists or partial agonists of GPCR polypeptides, which may
CC have therapeutic uses. The altered GPCRs may also be used in vivo or in
CC vitro in biological research. A nucleic acid encoding the altered GPCR
CC may be used to create a transgenic animal expressing the altered GPCR.
CC The method allows screening for compounds that modulate the activity of a
CC human G protein-coupled receptor without the need for provision of a
CC ligand for the receptor. This is particularly useful in allowing
CC screening of compounds against orphan receptors for which no ligand is
CC currently known. This sequence represents a human GPCR polypeptide of the
CC invention.
XX
SQ Sequence 378 AA;
XX
Query Match 99.2%; Score 1907; DB 7; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTVDYTLFESLCKKDVNRKAMP 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTVDYTLFESLCKKDVNRKAMP 60
QY 61 LPIWTSIIFGVGLNGVLVLTYYFKRKLTMTDTYLLMLAVADILFLTLPEWASAAK 120
Db 61 LPIWTSIIFGVGLNGVLVLTYYFKRKLTMTDTYLLMLAVADILFLTLPEWASAAK 120
QY 121 SWVFGVHFCKLIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRRARVLLISKLCV 180
Db 121 SWVFGVHFCKLIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRRARVLLISKLCV 180
QY 181 GSAILATVTSIBELLYSDLRSSSEQAMCSLITHEVEAFITTVQAVQNTIGPLVPLLAAS 240
Db 181 GSAILATVTSIBELLYSDLRSSSEQAMCSLITHEVEAFITTVQAVQNTIGPLVPLLAAS 240
QY 241 PCYLVIRTLQARNFERKAIKVIIVAVVVFIVFOLPYNQVLAQTVANFNITSSTCEL 300
Db 241 PCYLVIRTLQARNFERKAIKVIIVAVVVFIVFOLPYNQVLAQTVANFNITSSTCEL 300
QY 301 SKQLNIADVTYSLACVRCVNPFLYAFIGVFRNDIFKLFDGLGCLSQEQLRQSSCH 360
Db 301 SKQLNIADVTYSLACVRCVNPFLYAFIGVFRNDIFKLFDGLGCLSQEQLRQSSCH 360
QY 361 IRRSSMSVEAETTTTSP 378
Db 361 IRRSSMSVEAETTTTSP 378
XX
RESULT 13
ADH14066
XX ADH14066 standard; protein; 378 AA.
AC ADH14066;

XX 11-MAR-2004 (first entry)
DT Human ERI1.
XX
DE human; non-endogenous; G protein-coupled receptor; GPCR; receptor.
XX Homo sapiens.
XX OS US2003105292-A1.
XX
XX 05-JUN-2003.
XX
XX 20-SEP-2002; 2002US-00251385.
XX
XX 26-JUN-1998; 98US-0090783P.
XX 07-AUG-1998; 98US-0095677P.
XX 13-OCT-1998; 98US-00170496.
XX
XX (LIAW/) LIAW C W.
XX (BEHA/) BEHAN D P.
XX (CHAL/) CHALMERS D T.
XX
XX L1aw CW, Behan DP, Chalmers DT;
PI MPI; 2003-801247/75.
DR N-PSDB; ADH14065.
XX
PT New constitutively active, non-endogenous version of an endogenous human
PT G protein-coupled receptor for the identification of therapeutic
PT compounds, such as agonists.
XX
PS Example 1; SEQ ID NO 74; 227bp; English.
XX
CC The invention relates to a constitutively active, non-endogenous version
CC of an endogenous human G protein-coupled receptor (GPCR). The GPCR is
CC used for screening therapeutic compounds as inverse agonists, agonists or
CC partial agonists. The GPCR can be also be used to elucidate and
CC understand the roles of GPCRs in normal and diseased humans. The GPCR
CC need not be purified and isolated to be used to screen for therapeutic
CC compounds. The utility of the GPCR as a research tool is enhanced because
CC the role of a particular receptor can be understood before the endogenous
CC ligand is identified. The present sequence is used in the exemplification
CC of the present invention.
XX
SQ Sequence 378 AA;
XX
Query Match 99.2%; Score 1907; DB 7; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTVDYTLFESLCKKDVNRKAMP 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTVDYTLFESLCKKDVNRKAMP 60
QY 61 LPIWTSIIFGVGLNGVLVLTYYFKRKLTMTDTYLLMLAVADILFLTLPEWASAAK 120
Db 61 LPIWTSIIFGVGLNGVLVLTYYFKRKLTMTDTYLLMLAVADILFLTLPEWASAAK 120
QY 121 SWVFGVHFCKLIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRRARVLLISKLCV 180
Db 121 SWVFGVHFCKLIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHRRARVLLISKLCV 180
QY 181 GSAILATVTSIBELLYSDLRSSSEQAMCSLITHEVEAFITTVQAVQNTIGPLVPLLAAS 240
Db 181 GSAILATVTSIBELLYSDLRSSSEQAMCSLITHEVEAFITTVQAVQNTIGPLVPLLAAS 240
QY 241 PCYLVIRTLQARNFERKAIKVIIVAVVVFIVFOLPYNQVLAQTVANFNITSSTCEL 300
Db 241 PCYLVIRTLQARNFERKAIKVIIVAVVVFIVFOLPYNQVLAQTVANFNITSSTCEL 300
QY 301 SKQLNIADVTYSLACVRCVNPFLYAFIGVFRNDIFKLFDGLGCLSQEQLRQSSCH 360
Db 301 SKQLNIADVTYSLACVRCVNPFLYAFIGVFRNDIFKLFDGLGCLSQEQLRQSSCH 360

Db 301 SKQINAIADVITYSLACVRCNPPFLYAFIVGFKFRNDLFKLFKDLGCLSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
Db 361 IRRSSMSVEAETTTTFFSP 378
RESULT 14
ADH13199
ID ADH13199 standard; protein; 378 AA.
XX
AC ADH13199;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human malignant neoplasia-related protein Segid48.
XX
KM malignant neoplasia; cytostatic; breast cancer; ovarian cancer;
KM gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;
KM bladder cancer; non-small cell lung cancer; human.
XX
OS Homo sapiens.
XX
PN EP1365034-A2.
XX
PD 26-NOV-2003.
XX
PF 09-MAY-2003; 2003EP-00010447.
XX
PR 21-MAY-2002; 2002EP-00010291.
PR 13-FEB-2003; 2003EP-00003112.
XX
PA (FARB) BAYER AG.
XX
PI Wirtz R, Munnes M, Kallabis H;
XX
DR WPI; 2004-073279/08.
XX
DR N-PSDB; ADH13173.
XX
PT Predicting, diagnosing or prognosing malignant neoplasia by detecting at
PT least two markers, where the markers are genes from one or more
PT chromosomal regions altered in malignant neoplasia.
XX
PS Claim 11; SEQ ID NO 48; 267bp; English.
XX
XX This invention relates to a novel method for the prediction, diagnosis,
XX or prognosis of malignant neoplasia by the detection of at least two
XX markers. The invention may also be useful for the development of a
XX cyrostatic compounds through the regulation of the expression of a gene
XX or activity of a protein associated with malignant neoplasia. The method
XX is useful for prediction, diagnosis or prognosis of malignant neoplasia
XX such as breast cancer, ovarian cancer, gastric cancer, colon cancer,
XX oesophageal cancer, mesenchymal cancer, bladder cancer or non-small cell
XX lung cancer. The polynucleotides and polypeptides defined in the
XX specification, antisense polynucleotides targeting the polynucleotides,
XX antibodies targeting either one of the polynucleotides or polypeptides,
XX and compounds identified by the screening methods are useful for
XX preventing or treating malignant neoplasia. The disease treated is
XX preferably breast cancer. The present sequence is that of a human
XX malignant neoplasia-related protein which may be used in the method of
XX the invention.
XX
SQ Sequence 378 AA;
Query Match 99.2%; Score 1907; DB 8; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 61 LPIMYSIIICFVGLGNGLVLTLYIFPKLKTMTDTYLLNLAVADILFLTLTFPMAYSAK 120
QY 121 SWFGVHFCKLIIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSARRHARVLLISKLSKV 180
Db 121 SWFGVHFCKLIIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSARRHARVLLISKLSKV 180
QY 181 GSAILATVLSIPELLYSDLQRSSBQAMRGSLTBEHVEAFITTIQVQNVIGFLVPLAMS 240
Db 181 GIWILATVLSIPELLYSDLQRSSBQAMRGSLTBEHVEAFITTIQVQNVIGFLVPLAMS 240
QY 241 FCYLVITRTLLQARNFEENKAIKVIIVAVVFIPOLEPYNQVLAQTVANNTISSTCEL 300
Db 241 FCYLVITRTLLQARNFEENKAIKVIIVAVVFIPOLEPYNQVLAQTVANNTISSTCEL 300
QY 301 SKQINAIADVITYSLACVRCNPPFLYAFIVGFKFRNDLFKLFKDLGCLSOEQLRQWSSCRH 360
Db 301 SKQINAIADVITYSLACVRCNPPFLYAFIVGFKFRNDLFKLFKDLGCLSOEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
Db 361 IRRSSMSVEAETTTTFFSP 378
RESULT 15
ADO29231
ID ADO29231 standard; protein; 378 AA.
XX
AC ADO29231;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR CCR7, SEQ ID NO:332.
XX
KM G protein-coupled receptor; GPCR; drug screening; diagnosis;
KM transgenic mouse; neurological disorder; adrenal gland disorder;
KM colon disorder; intestinal disorder; cardiovascular disorder;
KM muscular disorder; blood disorder; immune disorder; bone disorder;
KM joint disorder; metabolic disorder; nutritive disorder; cancer;
KM kidney disorder; liver disorder; lung disorder; breast disorder;
KM ovary disorder; uterus disorder; prostate disorder; testis disorder;
KM skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KM thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KM cytostatic; antiinflammatory; vasotropic; antitanginal; antiarhythmic;
KM CNS; central nervous system; respiratory; antidiabetic;
KM vincristine; hepatotropic; antibacterial; antianaemic; antiepileptic;
KM dermatological; antitumor; antithyroid; antiallergic; anorectic;
KM immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
KM receptor.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
XX
PI Galitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
XX
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
DR WPI; 2004-390329/36.
DR N-PSDB; ADO29834.
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 332; 542bp; English.

CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridize to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 378 AA;

Query Match 99.2%; Score 1907; DB 8; Length 378;
Best Local Similarity 99.2%; Pred. No. 9.1e-205;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVITVQVCLCODEVDDYIGDNTTVDYTLFESLCSKKDYRNKAF 60
DB 1 MDLGRKMSVLLVALLVITVQVCLCODEVDDYIGDNTTVDYTLFESLCSKKDYRNKAF 60
QY 61 LPIWYSIICFVGILGGLVLTITVYFKRLKMTDTYLLNLAVADILFILTLPMFAYSAAK 120
DB 61 LPIWYSIICFVGILGGLVLTITVYFKRLKMTDTYLLNLAVADILFILTLPMFAYSAAK 120
QY 121 SWVFGVHFKCLIFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLSKV 180
DB 121 SWVFGVHFKCLIFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLSKV 180
QY 181 GSAILATVLSIPELLYSDLORSSSEQAMRCSLTTEHVEAFITTVQAQMTIGFLVPLIAMS 240
DB 181 GSAILATVLSIPELLYSDLORSSSEQAMRCSLTTEHVEAFITTVQAQMTIGFLVPLIAMS 240
QY 241 FCYLVIRITLLQARNERNKAIVITAVVVFIVPOLPYNGVLAQTVANFNITSSCEL 300
DB 241 FCYLVIRITLLQARNERNKAIVITAVVVFIVPOLPYNGVLAQTVANFNITSSCEL 300
QY 301 SKQLNIAYDVTSYLACVRCVNPFLYAFIGVKFRNDIFKLFKDLGCLSGEQLRQWSSCRH 360
DB 301 SKQLNIAYDVTSYLACVRCVNPFLYAFIGVKFRNDIFKLFKDLGCLSGEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378

Search completed: February 25, 2005, 02:19:57
Job time : 168 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: February 25, 2005, 02:15:02 ; Search time 43 Seconds
(without alignments)
656,217 Million cell updates/sec

Title: US-10-749-990-2

Perfect score: 1922

Sequence: 1 MDLGRKMSVLLVALLVIFQ.....RHRRSSMSVEAETTTTSP 378

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1932	100.0	378	1 US-08-383-750-2	Sequence 2, App1
2	1922	100.0	378	1 US-08-383-751A-2	Sequence 2, App1
3	1922	100.0	378	1 US-08-352-678-2	Sequence 2, App1
4	1922	100.0	378	4 US-09-445-583-49	Sequence 49, App1
5	1922	100.0	378	4 US-09-534-185-49	Sequence 49, App1
6	1922	100.0	378	4 US-09-536-954-2	Sequence 2, App1
7	1922	100.0	378	4 US-09-529-583B-2	Sequence 2, App1
8	1922	100.0	378	4 US-09-721-341-7	Sequence 7, App1
9	1922	100.0	378	4 US-09-721-495B-7	Sequence 7, App1
10	1922	100.0	378	5 PCT-US93-09636-2	Sequence 2, App1
11	1922	99.2	378	1 US-08-153-848-15	Sequence 15, App1
12	1907	99.2	378	3 US-09-299-843A-15	Sequence 15, App1
13	1907	99.2	378	3 US-09-251-545-1	Sequence 1, App1
14	1907	99.2	378	3 US-09-088-337B-15	Sequence 15, App1
15	1907	99.2	378	3 US-09-170-496D-74	Sequence 74, App1
16	1907	99.2	378	4 PCT-US93-11153-15	Sequence 15, App1
17	1900	98.9	378	4 US-09-170-496D-204	Sequence 204, App1
18	1814	94.4	410	1 US-08-153-848-7	Sequence 7, App1
19	1814	94.4	410	3 US-09-299-843A-7	Sequence 7, App1
20	1814	94.4	410	3 US-09-088-337B-7	Sequence 7, App1
21	1814	94.4	410	5 PCT-US93-11153-7	Sequence 7, App1
22	1813	94.3	358	1 US-08-153-848-19	Sequence 19, App1
23	1813	94.3	358	3 US-09-299-843A-19	Sequence 19, App1
24	1813	94.3	358	3 US-09-088-337B-19	Sequence 19, App1
25	1813	94.3	358	5 PCT-US93-11153-19	Sequence 19, App1
26	1795.5	93.4	361	3 US-08-302-294-2	Sequence 2, App1
27	1795.5	93.4	361	3 US-09-178-637-2	Sequence 2, App1

28	1696	88.2	378	3 US-09-299-843A-66	Sequence 66, App1
29	1696	88.2	378	1 US-09-088-337B-66	Sequence 66, App1
30	1602.5	83.4	359	3 US-08-153-848-24	Sequence 24, App1
31	1602.5	83.4	359	3 US-09-299-843A-24	Sequence 24, App1
32	1602.5	83.4	359	3 US-09-088-337B-24	Sequence 24, App1
33	1602.5	83.4	359	5 PCT-US93-11153-24	Sequence 24, App1
34	758.5	39.5	357	3 US-09-266-464-2	Sequence 2, App1
35	758.5	39.5	357	4 US-09-170-496D-24	Sequence 24, App1
36	758.5	39.5	357	4 US-09-952-385-2	Sequence 2, App1
37	758.5	39.5	369	4 US-09-721-341-6	Sequence 6, App1
38	758.5	39.5	369	4 US-09-721-495B-6	Sequence 6, App1
39	758.5	39.5	371	4 US-09-949-016-11223	Sequence 11223, A
40	753.5	39.2	357	4 US-09-170-496D-176	Sequence 176, App
41	753.5	39.2	369	4 US-09-826-509-481	Sequence 481, App
42	707.5	36.8	374	3 US-09-045-583-48	Sequence 48, App1
43	707.5	36.8	374	4 US-09-534-185-48	Sequence 48, App1
44	704.5	36.7	374	4 US-09-721-341-8	Sequence 8, App1
45	704.5	36.7	374	4 US-09-721-495B-8	Sequence 8, App1

ALIGNMENTS

```
RESULT 1
US-08-383-750-2
; Sequence 2, Application US/08383750
; Patent No. 5744301
; GENERAL INFORMATION:
; APPLICANT: Birkenbach, Mark
; TITLE OF INVENTION: Epstein Barr Virus Induced Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W.,
; STREET: Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,750
; FILING DATE: Herewith
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fox, Samuel, L.
; REGISTRATION NUMBER: 30,353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-383-750-2

Query Match 100.0%; Score 1922; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 MDLGRKMSVLLVALLVIFQVCLQDEVDYDGYDNTVDTLFEISCKKQDVRNFKAMP 60
DB 1 MDLGRKMSVLLVALLVIFQVCLQDEVDYDGYDNTVDTLFEISCKKQDVRNFKAMP 60
QY 61 LPIMSIIFVGLGNGLVLLTYIKRKLTMTDTYLLNLAVADIIFLLTLPFWASAAK 120

Db 61 LPIMTSICFVGLNGVLVLTYYIFKRLKMTDITYLNLAVADILFLTLTPEMAYSAK 120
QY 121 SWFGVHFCKLIIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db 121 SWFGVHFCKLIIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSAILATVLSIPELLYSIDLQRSSSQAMRCSLITHEVAFITTIQVAVNIGFLVPLAMS 240
Db 181 GSAILATVLSIPELLYSIDLQRSSSQAMRCSLITHEVAFITTIQVAVNIGFLVPLAMS 240
QY 241 FCYLVIRTLQARFERNKAIKVIAVVVFIVFQLPYNGVLAQTVANFNITSSTCEL 300
Db 241 FCYLVIRTLQARFERNKAIKVIAVVVFIVFQLPYNGVLAQTVANFNITSSTCEL 300
QY 301 SKQLNIADVITYSLACVRCNCPFLYAFIGVFRNDIFKLPDGLCGLSQEQLRQWSSCH 360
Db 301 SKQLNIADVITYSLACVRCNCPFLYAFIGVFRNDIFKLPDGLCGLSQEQLRQWSSCH 360
QY 361 IRRSSMSVEAETTTTTFSP 378
Db 361 IRRSSMSVEAETTTTTFSP 378

RESULT 2

US-08-383-751A-2
/ Sequence 2, Application US/08383751A
/ Patent No. 5753516
/ GENERAL INFORMATION:
/ APPLICANT: Heagy, Wyrta E.
/ APPLICANT: Finberg, Robert W.
/ TITLE OF INVENTION: Identification and Uses of Opioid
/ NUMBER OF INVENTION: Receptors
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: US
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/383,751A
/ FILING DATE: 03-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wilson, Mark B.
/ REGISTRATION NUMBER: 37,259
/ REFERENCE/DOCKET NUMBER: DPCI:001/WIM
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (512) 474-7577
/ TELEX: 79-0924
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 378 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-383-751A-2

Query Match 100.0%; Score 1922; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 1,7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGRKMSVSVLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRNPKAF 60
Db 1 MDLGRKMSVSVLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRNPKAF 60
QY 61 LPIMTSICFVGLNGVLVLTYYIFKRLKMTDITYLNLAVADILFLTLTPEMAYSAK 120

Db 61 LPIMTSICFVGLNGVLVLTYYIFKRLKMTDITYLNLAVADILFLTLTPEMAYSAK 120
QY 121 SWFGVHFCKLIIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db 121 SWFGVHFCKLIIPAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSAILATVLSIPELLYSIDLQRSSSQAMRCSLITHEVAFITTIQVAVNIGFLVPLAMS 240
Db 181 GSAILATVLSIPELLYSIDLQRSSSQAMRCSLITHEVAFITTIQVAVNIGFLVPLAMS 240
QY 241 FCYLVIRTLQARFERNKAIKVIAVVVFIVFQLPYNGVLAQTVANFNITSSTCEL 300
Db 241 FCYLVIRTLQARFERNKAIKVIAVVVFIVFQLPYNGVLAQTVANFNITSSTCEL 300
QY 301 SKQLNIADVITYSLACVRCNCPFLYAFIGVFRNDIFKLPDGLCGLSQEQLRQWSSCH 360
Db 301 SKQLNIADVITYSLACVRCNCPFLYAFIGVFRNDIFKLPDGLCGLSQEQLRQWSSCH 360
QY 361 IRRSSMSVEAETTTTTFSP 378
Db 361 IRRSSMSVEAETTTTTFSP 378

RESULT 3

US-08-352-678-2
/ Sequence 2, Application US/08352678
/ Patent No. 6043351
/ GENERAL INFORMATION:
/ APPLICANT: Birkenbach, Mark
/ APPLICANT: Kieff, Elliott
/ TITLE OF INVENTION: EBSTEIN BARR VIRUS INDUCED GENES
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Wolf, Greenfield & Sacks, P.C.
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patent in Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/352,678
/ FILING DATE: 30-NOV-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/980,518
/ FILING DATE: 25-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gates, Edward R.
/ REGISTRATION NUMBER: 31,616
/ REFERENCE/DOCKET NUMBER: B0801/7044
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-720-3500
/ TELEFAX: 617-720-2441
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 378 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-352-678-2

Query Match 100.0%; Score 1922; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 1,7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGRKMSVSVLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRNPKAF 60

Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDTYTLFESLCSKQDVNRKAMP 60
Qy 61 LPIMTSIIICFVGLGNGLVLLTYIYFKRLKMTDYLNLAVADILFLTLTPMAYSAK 120
Db 61 LPIMTSIIICFVGLGNGLVLLTYIYFKRLKMTDYLNLAVADILFLTLTPMAYSAK 120
Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQASAHHRARVLLISKLSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQASAHHRARVLLISKLSCV 180
Qy 181 GSAIIATVLSIBELYSIDQSSSEQAMRCSLITEHVAFTITQVQAWYIGFLVPLAMS 240
Db 181 GSAIIATVLSIBELYSIDQSSSEQAMRCSLITEHVAFTITQVQAWYIGFLVPLAMS 240
Qy 241 FCYLVIRTLQARNERNKAIKVIIVAVVFIQPLPYNQVLAQTVANFNITSSTCEL 300
Db 241 FCYLVIRTLQARNERNKAIKVIIVAVVFIQPLPYNQVLAQTVANFNITSSTCEL 300
Qy 301 SKQNLAYDVYTSIACVRCVNPFLYAFIGVKFRNDIFKLPDGLGCLSGEQLRQSSCRH 360
Db 301 SKQNLAYDVYTSIACVRCVNPFLYAFIGVKFRNDIFKLPDGLGCLSGEQLRQSSCRH 360
Qy 361 IRRSSMSVEAETTTTFSP 378
Db 361 IRRSSMSVEAETTTTFSP 378

RESULT 4

US-09-045-583-49
; Sequence 49, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNT-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-49

Query Match 100.0%; Score 1922; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 1,7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDTYTLFESLCSKQDVNRKAMP 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDTYTLFESLCSKQDVNRKAMP 60
Qy 61 LPIMTSIIICFVGLGNGLVLLTYIYFKRLKMTDYLNLAVADILFLTLTPMAYSAK 120
Db 61 LPIMTSIIICFVGLGNGLVLLTYIYFKRLKMTDYLNLAVADILFLTLTPMAYSAK 120
Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQASAHHRARVLLISKLSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQASAHHRARVLLISKLSCV 180
Qy 181 GSAIIATVLSIBELYSIDQSSSEQAMRCSLITEHVAFTITQVQAWYIGFLVPLAMS 240
Db 181 GSAIIATVLSIBELYSIDQSSSEQAMRCSLITEHVAFTITQVQAWYIGFLVPLAMS 240
Qy 241 FCYLVIRTLQARNERNKAIKVIIVAVVFIQPLPYNQVLAQTVANFNITSSTCEL 300
Db 241 FCYLVIRTLQARNERNKAIKVIIVAVVFIQPLPYNQVLAQTVANFNITSSTCEL 300
Qy 301 SKQNLAYDVYTSIACVRCVNPFLYAFIGVKFRNDIFKLPDGLGCLSGEQLRQSSCRH 360
Db 301 SKQNLAYDVYTSIACVRCVNPFLYAFIGVKFRNDIFKLPDGLGCLSGEQLRQSSCRH 360
Qy 361 IRRSSMSVEAETTTTFSP 378
Db 361 IRRSSMSVEAETTTTFSP 378

RESULT 5

US-09-534-185-49
; Sequence 49, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Hepthelical Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNT-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-534-185-49

Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
OY 61 LPIWTSIIICFVGLGNGLVLTYYIFKRLKTMTDYTLNLAVADILFLTLTPFMAYSAAK 120
DB 61 LPIWTSIIICFVGLGNGLVLTYYIFKRLKTMTDYTLNLAVADILFLTLTPFMAYSAAK 120
OY 121 SWFGVHFCKLIIFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKSCV 180
DB 121 SWFGVHFCKLIIFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKSCV 180
OY 181 GSALATVLSIPELLYSDLQSSSEQARCSLITHEVAFTITIOVAQWVIGFLVPLAMS 240
DB 181 GSALATVLSIPELLYSDLQSSSEQARCSLITHEVAFTITIOVAQWVIGFLVPLAMS 240
OY 241 FCYLVITRLQARNFERKAIKVIIAAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVITRLQARNFERKAIKVIIAAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
OY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFQLFDLQCLSOEOLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFQLFDLQCLSOEOLRQWSSCRH 360
OY 361 IRRSSMSVBAETTTTFSP 378
DB 361 IRRSSMSVBAETTTTFSP 378
```

RESULT 6

US-09-536-954-2
Sequence 2, Application US/09536954
Patent No. 6500926

GENERAL INFORMATION:
APPLICANT: Birkbach, Mark
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/352,678
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-536-954-2

Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
OY 61 LPIWTSIIICFVGLGNGLVLTYYIFKRLKTMTDYTLNLAVADILFLTLTPFMAYSAAK 120
DB 61 LPIWTSIIICFVGLGNGLVLTYYIFKRLKTMTDYTLNLAVADILFLTLTPFMAYSAAK 120
OY 121 SWFGVHFCKLIIFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKSCV 180
DB 121 SWFGVHFCKLIIFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISKSCV 180
OY 181 GSALATVLSIPELLYSDLQSSSEQARCSLITHEVAFTITIOVAQWVIGFLVPLAMS 240
DB 181 GSALATVLSIPELLYSDLQSSSEQARCSLITHEVAFTITIOVAQWVIGFLVPLAMS 240
OY 241 FCYLVITRLQARNFERKAIKVIIAAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVITRLQARNFERKAIKVIIAAVVVFIVFQLPYNGVLAQTVANFNITSTCEL 300
OY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFQLFDLQCLSOEOLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFQLFDLQCLSOEOLRQWSSCRH 360
OY 361 IRRSSMSVBAETTTTFSP 378
DB 361 IRRSSMSVBAETTTTFSP 378
```

RESULT 7

US-09-929-583B-2
Sequence 2, Application US/09929583B
Patent No. 6699971

GENERAL INFORMATION:
APPLICANT: Birkbach, Mark
TITLE OF INVENTION: ANTIBODIES THAT BIND EPSTEIN BARR VIRUS INDUCED PROTEINS
FILE REFERENCE: B0801.70226US00
CURRENT APPLICATION NUMBER: US/09/929,583B
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 09/536,954
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: US 08/352,678
PRIOR FILING DATE: 1994-11-30
PRIOR APPLICATION NUMBER: US 07/980,518
PRIOR FILING DATE: 1992-11-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-09-929-583B-2

Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKKQVRNFKAMF 60
OY 61 LPIWTSIIICFVGLGNGLVLTYYIFKRLKTMTDYTLNLAVADILFLTLTPFMAYSAAK 120
```

```
Db 61 LPIWMSIICFVGLGGLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFWAYSAAK 120
Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Qy 181 GSAILATVSIPELLYSDIQRSSSEQAMRCSLITEHVEAFITIQVQWYIGFLVPLLAWS 240
Db 181 GSAILATVSIPELLYSDIQRSSSEQAMRCSLITEHVEAFITIQVQWYIGFLVPLLAWS 240
Qy 241 FCYLVIRTLQARNERNKAIKVIAVWVFIVFQLPYNGVVLAAQTVAINFITSTCEL 300
Db 241 FCYLVIRTLQARNERNKAIKVIAVWVFIVFQLPYNGVVLAAQTVAINFITSTCEL 300
Qy 301 SKQMLNAYDVVTSYSLACVRCVNPFLYAFYGVKFRNDIFKLFDLGLCSOQLRQWSSCRH 360
Db 301 SKQMLNAYDVVTSYSLACVRCVNPFLYAFYGVKFRNDIFKLFDLGLCSOQLRQWSSCRH 360
Qy 361 IRRSSMSVEAETTTTFSP 378
Db 361 IRRSSMSVEAETTTTFSP 378
```

```
RESULT 8
US-09-721-341-7
; Sequence 7, Application US/09721341
; Patent No. 6828108
; GENERAL INFORMATION:
; APPLICANT: Goelling, Jennife
; APPLICANT: Dairegh, Daniel J.
; APPLICANT: Hanley, Michael
; APPLICANT: Miao, Zhenhua
; APPLICANT: Schall, Thomas J.
; APPLICANT: ChemoCentryx, Inc.
; TITLE OF INVENTION: Chemokine Receptor
; FILE REFERENCE: 019934-000710US
; CURRENT APPLICATION NUMBER: US/09/721,341
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/686,020
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/159,015
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 60/159,210
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/172,979
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/173,388
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/186,626
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: chemokine receptor (CCR7)
US-09-721-341-7
```

```
Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTYDYTLFESLCSKQDVNRKAMP 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTYDYTLFESLCSKQDVNRKAMP 60
Qy 61 LPIWMSIICFVGLGGLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFWAYSAAK 120
Db 61 LPIWMSIICFVGLGGLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFWAYSAAK 120
```

```
Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Qy 181 GSAILATVSIPELLYSDIQRSSSEQAMRCSLITEHVEAFITIQVQWYIGFLVPLLAWS 240
Db 181 GSAILATVSIPELLYSDIQRSSSEQAMRCSLITEHVEAFITIQVQWYIGFLVPLLAWS 240
Qy 241 FCYLVIRTLQARNERNKAIKVIAVWVFIVFQLPYNGVVLAAQTVAINFITSTCEL 300
Db 241 FCYLVIRTLQARNERNKAIKVIAVWVFIVFQLPYNGVVLAAQTVAINFITSTCEL 300
Qy 301 SKQMLNAYDVVTSYSLACVRCVNPFLYAFYGVKFRNDIFKLFDLGLCSOQLRQWSSCRH 360
Db 301 SKQMLNAYDVVTSYSLACVRCVNPFLYAFYGVKFRNDIFKLFDLGLCSOQLRQWSSCRH 360
Qy 361 IRRSSMSVEAETTTTFSP 378
Db 361 IRRSSMSVEAETTTTFSP 378
```

```
RESULT 9
US-09-721-495B-7
; Sequence 7, Application US/09721495B
; Patent No. 6835547
; GENERAL INFORMATION:
; APPLICANT: Goelling, Jennife
; APPLICANT: Dairegh, Daniel J.
; APPLICANT: Hanley, Michael
; APPLICANT: Miao, Zhenhua
; APPLICANT: Talbot, Dale
; APPLICANT: Schall, Thomas J.
; APPLICANT: ChemoCentryx, Inc.
; TITLE OF INVENTION: Chemokine Receptor
; FILE REFERENCE: 019934-0007210US
; CURRENT APPLICATION NUMBER: US/09/721,495B
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/159,015
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US 60/159,210
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/172,979
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/173,388
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/186,626
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 09/686,019
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: chemokine receptor CCR7
US-09-721-495B-7
```

```
Query Match 100.0%; Score 1922; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTYDYTLFESLCSKQDVNRKAMP 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGDNTTYDYTLFESLCSKQDVNRKAMP 60
Qy 61 LPIWMSIICFVGLGGLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFWAYSAAK 120
Db 61 LPIWMSIICFVGLGGLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFWAYSAAK 120
Qy 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
Db 121 SWFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRRARVLLISLSCV 180
```

Db 121 SWFGVHECKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSALATATVLSIPPELLYSDLQRRSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
Db 181 GSALATATVLSIPPELLYSDLQRRSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
QY 241 FCYLVITITLLQARNPERKAIKVIIAAVVVFIQFOLPYNQVLAQTVANFNITSTCEL 300
Db 241 FCYLVITITLLQARNPERKAIKVIIAAVVVFIQFOLPYNQVLAQTVANFNITSTCEL 300
QY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDJGCLSQEQLRQWSSCRH 360
Db 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDJGCLSQEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
Db 361 IRRSSMSVEAETTTTFSP 378

RESULT 10

PCT-US93-09636-2
Sequence 2, Application PC/TUS9309636
GENERAL INFORMATION:
APPLICANT: Birkbach, Mark
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09636
FILING DATE: herewith
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-09636-2

Query Match 100.0%; Score 1922; DB 5; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.7e-153;

Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGDNTVDYTLFESLCSKQDVRFKAMF 60
Db 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGDNTVDYTLFESLCSKQDVRFKAMF 60
QY 61 LPIMYSIICFVGLGNGLVLTYYIFKRLKTMVTDYLLNLAAVADILFLTLTFPMAYSAK 120
Db 61 LPIMYSIICFVGLGNGLVLTYYIFKRLKTMVTDYLLNLAAVADILFLTLTFPMAYSAK 120
QY 121 SWFGVHPECKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db 121 SWFGVHPECKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
QY 181 GSALATATVLSIPPELLYSDLQRRSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240
Db 181 GSALATATVLSIPPELLYSDLQRRSSSQAMRCSLITEHVEAFITIOVAQWVIGFLVPLAMS 240

QY 241 FCYLVITITLLQARNPERKAIKVIIAAVVVFIQFOLPYNQVLAQTVANFNITSTCEL 300
Db 241 FCYLVITITLLQARNPERKAIKVIIAAVVVFIQFOLPYNQVLAQTVANFNITSTCEL 300
QY 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDJGCLSQEQLRQWSSCRH 360
Db 301 SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLFDJGCLSQEQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
Db 361 IRRSSMSVEAETTTTFSP 378

RESULT 11

US-08-153-848-15
Sequence 15, Application US/08153848
Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-15

Query Match 99.2%; Score 1907; DB 1; Length 378;
Best Local Similarity 99.2%; Pred. No. 3.1e-152;

Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGDNTVDYTLFESLCSKQDVRFKAMF 60
Db 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGDNTVDYTLFESLCSKQDVRFKAMF 60
QY 61 LPIMYSIICFVGLGNGLVLTYYIFKRLKTMVTDYLLNLAAVADILFLTLTFPMAYSAK 120
Db 61 LPIMYSIICFVGLGNGLVLTYYIFKRLKTMVTDYLLNLAAVADILFLTLTFPMAYSAK 120
QY 121 SWFGVHECKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180
Db 121 SWFGVHECKLIFAIYKMSFSGMLLLCISIDRYVAIVQAVSAHRHARVLLISKSCV 180

Db 121 SWFGVHFCKLFAIYKMSFSGMILLICISIDRYVAIVQASAHRRARVLLISKSCV 180
QY 181 GSAIATVLSIBELYSIDQSSSEQAMRCSLITHEVEAFITTOVQOMVIGFLVPLLAAS 240
Db 181 GIMILATVLSIBELYSIDQSSSEQAMRCSLITHEVEAFITTOVQOMVIGFLVPLLAAS 240
QY 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFOLPYNGVVLQOTVANFNITSTCEL 300
Db 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFOLPYNGVVLQOTVANFNITSTCEL 300
QY 301 SKQNLNAYDVYSLACVRCVNPFLYAFIGVFRNDIFKLFKDLGCLSGEOLQWSSCRH 360
Db 301 SKQNLNAYDVYSLACVRCVNPFLYAFIGVFRNDIFKLFKDLGCLSGEOLQWSSCRH 360
QY 361 IRRSSMSVEAETTTTTFSP 378
Db 361 IRRSSMSVEAETTTTTFSP 378

RESULT 12
US-09-299-843A-15
Sequence 15. Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schwellhart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-15

Query Match 99.2%; Score 1907; DB 3; Length 378;
Best Local Similarity 99.2%; Pred. No. 3.1e-152;

Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDGKPMKSVLVVALLVIFOVCLCODEVTDDYIGNTTVDYTLFESLCSKRDVRFKAMP 60
Db 1 MDGKPMKSVLVVALLVIFOVCLCODEVTDDYIGNTTVDYTLFESLCSKRDVRFKAMP 60
QY 61 LPIWYSIICFVGILGNGVLVLTYYIKRLKMTDYLNLAVADILFLTLPPWASAAK 120
Db 61 LPIWYSIICFVGILGNGVLVLTYYIKRLKMTDYLNLAVADILFLTLPPWASAAK 120
QY 121 SWFGVHFCKLFAIYKMSFSGMILLICISIDRYVAIVQASAHRRARVLLISKSCV 180
Db 121 SWFGVHFCKLFAIYKMSFSGMILLICISIDRYVAIVQASAHRRARVLLISKSCV 180
QY 181 GSAIATVLSIBELYSIDQSSSEQAMRCSLITHEVEAFITTOVQOMVIGFLVPLLAAS 240
Db 181 GIMILATVLSIBELYSIDQSSSEQAMRCSLITHEVEAFITTOVQOMVIGFLVPLLAAS 240
QY 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFOLPYNGVVLQOTVANFNITSTCEL 300
Db 241 FCYLVIIIRTLQARNFERNKAIKVIIVVVFIVFOLPYNGVVLQOTVANFNITSTCEL 300
QY 301 SKQNLNAYDVYSLACVRCVNPFLYAFIGVFRNDIFKLFKDLGCLSGEOLQWSSCRH 360
Db 301 SKQNLNAYDVYSLACVRCVNPFLYAFIGVFRNDIFKLFKDLGCLSGEOLQWSSCRH 360
QY 361 IRRSSMSVEAETTTTTFSP 378
Db 361 IRRSSMSVEAETTTTTFSP 378

RESULT 13
US-09-251-545-1
Sequence 1. Application US/09251545
Patent No. 6154441
GENERAL INFORMATION:
APPLICANT: Edward R. Appelbaum
APPLICANT: Henry M. Sarau
APPLICANT: John R. White
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
AND CK-9 LIGAND AND INTERACTION THEREOF
FILE REFERENCE: P50753
CURRENT APPLICATION NUMBER: US/09/251,545
EARLIER FILING DATE: 1999-02-17
EARLIER APPLICATION NUMBER: 60/074,883
EARLIER FILING DATE: 1998-02-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for windows Version 3.0
SEQ ID NO 1
LENGTH: 378
TYPE: PRT
ORGANISM: Human
US-09-251-545-1

Query Match 99.2%; Score 1907; DB 3; Length 378;
Best Local Similarity 99.2%; Pred. No. 3.1e-152;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDGKPMKSVLVVALLVIFOVCLCODEVTDDYIGNTTVDYTLFESLCSKRDVRFKAMP 60
Db 1 MDGKPMKSVLVVALLVIFOVCLCODEVTDDYIGNTTVDYTLFESLCSKRDVRFKAMP 60
QY 61 LPIWYSIICFVGILGNGVLVLTYYIKRLKMTDYLNLAVADILFLTLPPWASAAK 120
Db 61 LPIWYSIICFVGILGNGVLVLTYYIKRLKMTDYLNLAVADILFLTLPPWASAAK 120
QY 121 SWFGVHFCKLFAIYKMSFSGMILLICISIDRYVAIVQASAHRRARVLLISKSCV 180
Db 121 SWFGVHFCKLFAIYKMSFSGMILLICISIDRYVAIVQASAHRRARVLLISKSCV 180
QY 181 GSAIATVLSIBELYSIDQSSSEQAMRCSLITHEVEAFITTOVQOMVIGFLVPLLAAS 240
Db 181 GIMILATVLSIBELYSIDQSSSEQAMRCSLITHEVEAFITTOVQOMVIGFLVPLLAAS 240

Db 181 GIMILATVLSIPELLYSDLRSSSQAMRCSLITEHVEAFITIQVAQWIGFLVPLAMS 240
Qy 241 FCYLVITIRTLQARNPERKKAIVIAVAVVFIQVLPYNGVLAQTVANFNITSSCEL 300
Db 241 FCYLVITIRTLQARNPERKKAIVIAVAVVFIQVLPYNGVLAQTVANFNITSSCEL 300
Qy 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLPFDLGLCSQEQRLQWSSCGH 360
Db 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLPFDLGLCSQEQRLQWSSCGH 360
Qy 361 IRRSSMSVEAETTTTTFSP 378
Db 361 IRRSSMSVEAETTTTTFSP 378

RESULT 14
US-09-088-337B-15
; Sequence 15, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Gray, Patrick W.
; Schweiart, Vicki L.
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borum
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-088-337B-15

Query Match 99.2%; Score 1907; DB 3; Length 378;
Best Local Similarity 99.2%; Pred. No. 3.1e-152;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKQDVRNFKAF 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKQDVRNFKAF 60
Qy 61 LPIMTSIIICFVGLDNGLVLTLYIFKRLKMTDITYLNLAAVADILFLTLTFFMAISA 120

Db 61 LPIMTSIIICFVGLDNGLVLTLYIFKRLKMTDITYLNLAAVADILFLTLTFFMAISA 120
Qy 121 SWVFGVHCKLIFAIYKNSPFGMLLLCISIDRYVAIVQASARHRRARVLLISKLSGV 180
Db 121 SWVFGVHCKLIFAIYKNSPFGMLLLCISIDRYVAIVQASARHRRARVLLISKLSGV 180
Qy 181 GSAILIATVLSIPELLYSDLRSSSQAMRCSLITEHVEAFITIQVAQWIGFLVPLAMS 240
Db 181 GIMILATVLSIPELLYSDLRSSSQAMRCSLITEHVEAFITIQVAQWIGFLVPLAMS 240
Qy 241 FCYLVITIRTLQARNPERKKAIVIAVAVVFIQVLPYNGVLAQTVANFNITSSCEL 300
Db 241 FCYLVITIRTLQARNPERKKAIVIAVAVVFIQVLPYNGVLAQTVANFNITSSCEL 300
Qy 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLPFDLGLCSQEQRLQWSSCGH 360
Db 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLPFDLGLCSQEQRLQWSSCGH 360
Qy 361 IRRSSMSVEAETTTTTFSP 378
Db 361 IRRSSMSVEAETTTTTFSP 378

RESULT 15
US-09-170-496D-74
; Sequence 74, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-(
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 74
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-74

Query Match 99.2%; Score 1907; DB 4; Length 378;
Best Local Similarity 99.2%; Pred. No. 3.1e-152;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKQDVRNFKAF 60
Db 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTVDYTLFBSLCSKQDVRNFKAF 60
Qy 61 LPIMTSIIICFVGLDNGLVLTLYIFKRLKMTDITYLNLAAVADILFLTLTFFMAISA 120
Db 61 LPIMTSIIICFVGLDNGLVLTLYIFKRLKMTDITYLNLAAVADILFLTLTFFMAISA 120
Qy 121 SWVFGVHCKLIFAIYKNSPFGMLLLCISIDRYVAIVQASARHRRARVLLISKLSGV 180
Db 121 SWVFGVHCKLIFAIYKNSPFGMLLLCISIDRYVAIVQASARHRRARVLLISKLSGV 180
Qy 181 GSAILIATVLSIPELLYSDLRSSSQAMRCSLITEHVEAFITIQVAQWIGFLVPLAMS 240
Db 181 GIMILATVLSIPELLYSDLRSSSQAMRCSLITEHVEAFITIQVAQWIGFLVPLAMS 240
Qy 241 FCYLVITIRTLQARNPERKKAIVIAVAVVFIQVLPYNGVLAQTVANFNITSSCEL 300
Db 241 FCYLVITIRTLQARNPERKKAIVIAVAVVFIQVLPYNGVLAQTVANFNITSSCEL 300
Qy 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLPFDLGLCSQEQRLQWSSCGH 360
Db 301 SKQNLIAVDVYSLACVRCVNPFLYAFIGVFRNDIFKLPFDLGLCSQEQRLQWSSCGH 360

Oy	361	IRSSMSVEAETTTTSP	378
Db	361	IRSSMSVEAETTTTSP	378

Search completed: February 25, 2005, 02:24:33
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using BW model

Run on: February 25, 2005, 02:23:03 ; Search time 134 Seconds

(without alignments)
923.113 Million cell updates/sec

Title: US-10-749-990-2

Perfect score: 1 MDLGRPKSVLWVALLVIFQ.....RHRRSSMSVEAETTTTSP 378

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/PCTUS_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1922	100.0	378	9	US-09-929-583B-2
2	1922	100.0	378	14	US-10-164-649-49
3	1922	100.0	378	16	US-10-749-990-2
4	1907	99.2	378	14	US-10-251-385-74
5	1907	99.2	378	14	US-10-225-567A-68
6	1907	99.2	378	14	US-10-239-423-70
7	1907	99.2	378	15	US-10-435-696-48
8	1900	98.9	378	14	US-10-251-385-204
9	1814	94.4	475	15	US-10-425-114-56811
10	758.5	39.5	357	9	US-09-903-377-2
11	758.5	39.5	357	9	US-09-952-385-2
12	758.5	39.5	357	10	US-09-966-755-2
13	758.5	39.5	357	13	US-10-000-759A-2

14	758.5	39.5	357	14	US-10-251-385-24	Sequence 24, App1
15	758.5	39.5	357	14	US-10-225-567A-241	Sequence 241, App
16	758.5	39.5	357	14	US-10-239-423-73	Sequence 73, App1
17	758.5	39.5	369	14	US-10-239-423-72	Sequence 72, App1
18	753.5	39.2	357	14	US-10-251-385-176	Sequence 176, App
19	753.5	39.2	369	10	US-09-825-509-481	Sequence 481, App
20	753.5	39.2	369	17	US-10-925-095-481	Sequence 481, App
21	707.5	36.8	369	14	US-10-239-423-69	Sequence 69, App1
22	707.5	36.8	374	14	US-10-164-649-48	Sequence 48, App1
23	707.5	36.8	374	14	US-10-239-423-68	Sequence 68, App1
24	707.5	36.8	390	13	US-10-087-192-1920	Sequence 1920, Ap
25	707.5	36.8	406	14	US-10-325-430-18	Sequence 18, App1
26	707.5	36.8	406	14	US-10-029-386-32911	Sequence 32911, A
27	704.5	36.7	374	14	US-10-225-567A-390	Sequence 390, App
28	703	36.6	367	14	US-10-254-089-2	Sequence 2, App11
29	703	36.6	408	13	US-10-244-089-2	Sequence 2, App11
30	703	36.6	408	13	US-10-087-192-1917	Sequence 1917, Ap
31	664	34.5	365	15	US-10-643-431-8	Sequence 8, App11
32	663	34.5	365	15	US-10-039-659-10	Sequence 10, App1
33	663	34.5	365	16	US-10-754-071-10	Sequence 10, App1
34	650	33.8	350	10	US-09-910-695-8	Sequence 8, App11
35	643	33.5	350	9	US-09-765-994-2	Sequence 2, App11
36	643	33.5	350	9	US-09-796-338A-8	Sequence 8, App11
37	643	33.5	350	10	US-09-966-433-16	Sequence 16, App1
38	643	33.5	350	14	US-10-282-837-8	Sequence 8, App11
39	643	33.5	350	14	US-10-225-567A-607	Sequence 607, App
40	643	33.5	350	14	US-10-288-222A-10	Sequence 10, App1
41	643	33.5	350	14	US-10-145-586-8	Sequence 8, App11
42	643	33.5	350	14	US-10-239-423-75	Sequence 75, App1
43	643	33.5	350	15	US-10-407-079-84	Sequence 84, App1
44	642	33.4	348	15	US-10-403-161-12	Sequence 12, App1
45	642	33.4	349	9	US-09-765-994-4	Sequence 4, App11

ALIGNMENTS

US-09-929-583B-2	US-10-251-385-24
1	1
US-09-929-583B-2	US-10-225-567A-241
1	1
US-09-929-583B-2	US-10-239-423-73
1	1
US-09-929-583B-2	US-10-239-423-72
1	1
US-09-929-583B-2	US-10-251-385-176
1	1
US-09-929-583B-2	US-10-825-509-481
1	1
US-09-929-583B-2	US-10-925-095-481
1	1
US-09-929-583B-2	US-10-239-423-69
1	1
US-09-929-583B-2	US-10-164-649-48
1	1
US-09-929-583B-2	US-10-239-423-68
1	1
US-09-929-583B-2	US-10-087-192-1920
1	1
US-09-929-583B-2	US-10-325-430-18
1	1
US-09-929-583B-2	US-10-029-386-32911
1	1
US-09-929-583B-2	US-10-225-567A-390
1	1
US-09-929-583B-2	US-10-254-089-2
1	1
US-09-929-583B-2	US-10-244-089-2
1	1
US-09-929-583B-2	US-10-087-192-1917
1	1
US-09-929-583B-2	US-10-643-431-8
1	1
US-09-929-583B-2	US-10-039-659-10
1	1
US-09-929-583B-2	US-10-754-071-10
1	1
US-09-929-583B-2	US-09-910-695-8
1	1
US-09-929-583B-2	US-09-765-994-2
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	US-09-796-338A-8
1	1
US-09-929-583B-2	US-09-966-433-16
1	1
US-09-929-583B-2	US-10-282-837-8
1	1
US-09-929-583B-2	US-10-225-567A-607
1	1
US-09-929-583B-2	US-10-288-222A-10
1	1
US-09-929-583B-2	US-10-145-586-8
1	1
US-09-929-583B-2	US-10-239-423-75
1	1
US-09-929-583B-2	US-10-407-079-84
1	1
US-09-929-583B-2	US-10-403-161-12
1	1
US-09-929-583B-2	US-09-765-994-4
1	1
US-09-929-583B-2	

QY 121 SWFGVHFCCKLIPALYKXSPFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
DB 121 SWFGVHFCCKLIPALYKXSPFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
QY 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIOVAQWVIGFLVPLLAMS 240
DB 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIOVAQWVIGFLVPLLAMS 240
QY 241 FCYLVITIRTLQARNFERNKAIKVIAVAVVFIQOLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVITIRTLQARNFERNKAIKVIAVAVVFIQOLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQINIAVDVYSLACVRCNPFYAFIGVKFRNDIFKLFQDLGCLSOEOLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCNPFYAFIGVKFRNDIFKLFQDLGCLSOEOLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

RESULT 2

US-10-164-649-49
Sequence 49, Application US/10164649
Publication No. US20030162943A1
GENERAL INFORMATION:
APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. US20030162943A1 Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
CITY: Boston
STREET: 28 State Street
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/164,649
FILING DATE: 07-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/045,583
FILING DATE: 20-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MNI-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-164-649-49

Query Match 100.0%; Score 1922; DB 14; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.3e-158;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSKQDVARNFKAMF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSKQDVARNFKAMF 60

QY 61 LPIMYSIIICFVGLGNGVLTYYIFKRLKTMPTDYTLNLAVADTLFLLTLPFMAYSAAK 120
DB 61 LPIMYSIIICFVGLGNGVLTYYIFKRLKTMPTDYTLNLAVADTLFLLTLPFMAYSAAK 120
QY 121 SWFGVHFCCKLIPALYKXSPFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
DB 121 SWFGVHFCCKLIPALYKXSPFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
QY 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIOVAQWVIGFLVPLLAMS 240
DB 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIOVAQWVIGFLVPLLAMS 240
QY 241 FCYLVITIRTLQARNFERNKAIKVIAVAVVFIQOLPYNGVLAQTVANFNITSTCEL 300
DB 241 FCYLVITIRTLQARNFERNKAIKVIAVAVVFIQOLPYNGVLAQTVANFNITSTCEL 300
QY 301 SKQINIAVDVYSLACVRCNPFYAFIGVKFRNDIFKLFQDLGCLSOEOLRQWSSCRH 360
DB 301 SKQINIAVDVYSLACVRCNPFYAFIGVKFRNDIFKLFQDLGCLSOEOLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

RESULT 3

US-10-749-990-2
Sequence 2, Application US/10749990
Publication No. US20040138418A1
GENERAL INFORMATION:
APPLICANT: Birkendach, Mark
APPLICANT: Kieft, Elliot
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
FILE REFERENCE: B0801.70226US01
CURRENT APPLICATION NUMBER: US/10/749,990
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 09/929,583
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 09/536,954
PRIOR FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: US 08/352,678
PRIOR FILING DATE: 1994-11-30
PRIOR APPLICATION NUMBER: US 07/980,518
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-10-749-990-2

Query Match 100.0%; Score 1922; DB 16; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.3e-158;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSKQDVARNFKAMF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLSKQDVARNFKAMF 60
QY 61 LPIMYSIIICFVGLGNGVLTYYIFKRLKTMPTDYTLNLAVADTLFLLTLPFMAYSAAK 120
DB 61 LPIMYSIIICFVGLGNGVLTYYIFKRLKTMPTDYTLNLAVADTLFLLTLPFMAYSAAK 120
QY 121 SWFGVHFCCKLIPALYKXSPFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
DB 121 SWFGVHFCCKLIPALYKXSPFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
QY 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIOVAQWVIGFLVPLLAMS 240
DB 181 GSAILATVLSIPELLYSDLQRSSSEQAMRCSLITEHVEAFITIOVAQWVIGFLVPLLAMS 240

Qy	241	FCYVITRTLLQANFEENKAIKVIIAVVWFIVQLPNGVLAQTANFNITSTCEL	300
	241	FCYVITRTLLQANFEENKAIKVIIAVVWFIVQLPNGVLAQTANFNITSTCEL	300
Db	241	FCYVITRTLLQANFEENKAIKVIIAVVWFIVQLPNGVLAQTANFNITSTCEL	300
Qy	301	SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFCLFDLGLCSQQLRQSSCRH	360
	301	SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFCLFDLGLCSQQLRQSSCRH	360
Db	301	SKQINIAVDVYSLACVRCVNPFLYAFIGVFRNDIFCLFDLGLCSQQLRQSSCRH	360
Qy	361	IRRSMSVEAETTTTFFSP	378
	361	IRRSMSVEAETTTTFFSP	378
Db	361	IRRSMSVEAETTTTFFSP	378

```

RESULT 4
US-10-251-385-74
; Sequence 74, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; TITLE OF INVENTION: L1w, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 378
; TYPE: prt
; ORGANISM: Homo sapiens
; US-10-251-385-74

```

Query Match	99.2%	Score 1907	DB 14	Length 378
Best Local Similarity	99.2%	Pred. No. 4.6e-157		
Matches 375, Conservative	1	Mismatches 2	Indels 0	Gaps 0

Qy	1	MDLCKPMKSVLVAALLVLFVQVCLCODEVTDVYIGDNTTVDYTLFESLCKSKDVRPKAMF	60
Dd	1	MDLCKPMKSVLVAALLVLFVQVCLCODEVTDVYIGDNTTVDYTLFESLCKSKDVRPKAMF	60
Qy	61	LPIMYSIICFVGLGNGLVLTLYIYFKRLKTMTDYTLNLNAVADLLFLITLTFPMYASAK	120
Dd	61	LPIMYSIICFVGLGNGLVLTLYIYFKRLKTMTDYTLNLNAVADLLFLITLTFPMYASAK	120
Qy	121	SMVGVMFHCKLIFALYKMSFPGMMLLICI SIDRVAVIQAASAHRRHARULLISKLSCV	180
Dd	121	SMVGVMFHCKLIFALYKMSFPGMMLLICI SIDRVAVIQAASAHRRHARULLISKLSCV	180
Qy	181	GSALILATYLSIPBLLYSDLORSSSEQAMRCSLITEHVEAFITIOVAQWIGFVLPLIAMS	240
Dd	181	GIMILATYLSIPBLLYSDLORSSSEQAMRCSLITEHVEAFITIOVAQWIGFVLPLIAMS	240
Qy	241	FCYLVIIKRTLQARNFERNKAIKVIIAAVVVEIVFQLPNGVVLAQTVANFNITSCTEL	300
Dd	241	FCYLVIIKRTLQARNFERNKAIKVIIAAVVVEIVFQLPNGVVLAQTVANFNITSCTEL	300
Qy	301	SKOLNIADVTVYSLACVRCVCNPFILAFIYGVKFRNDIFELFQDLGCLSOQLRQWSSCH	360
Dd	301	SKOLNIADVTVYSLACVRCVCNPFILAFIYGVKFRNDIFELFQDLGCLSOQLRQWSSCH	360
Qy	361	IRRSSMSVEAEETTTTFFSP	378
Dd	361	IRRSSMSVEAEETTTTFFSP	378

RESULT 5
US-10-225-567A-68
; Sequence 68, Application US/10225567A

```

: Publication No. US20030113798A1
: GENERAL INFORMATION:
: APPLICANT: Lifespan Biosciences
: APPLICANT: Brown, Joseph P.
: APPLICANT: Burnet, Glenn A.
: APPLICANT: Roush, Christine L.
: TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
: FILE REFERENCE: 1920--4-4
: CURRENT APPLICATION NUMBER: US/10/225,567A
: CURRENT FILING DATE: 2001-12-19
: PRIOR APPLICATION NUMBER: 60/257,144
: PRIOR FILING DATE: 2000-12-19
: NUMBER OF SEQ ID NOS: 2292
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 68
: LENGTH: 378
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-225-567A-68

```

Query Match	99.2%	Score 1907;	DB 14	Length 378;
Best Local Similarity	99.2%	Pred. No. 4.6e-157;		
Matches 375;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0

Qy	1	MGGKPKMSVLAVALVITFOVCLCODEVTDYDYGDMTTVDYTLFESLCSKQDVRNPFAMF	60
Db	1	MDJGKPKMSVLAVALVITFOVCLCODEVTDYDYGDMTTVDYTLFESLCSKQDVRNPFAMF	60
Qy	61	LPIMYSIICFVGLLGNGLVVLTYIYFKRLKTMTDYTLNLNAVADILFLLTLPFWAASA	120
Db	61	LPIMYSIICFVGLLGNGLVVLTYIYFKRLKTMTDYTLNLNAVADILFLLTLPFWAASA	120
Qy	121	SWPFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYAIVQAVSAHRHRAVLLISKLS	180
Db	121	SWPFGVHFCKLIPAIYKMSFFSGMLLLCISIDRYAIVQAVSAHRHRAVLLISKLS	180
Qy	181	GSNIILATVLSIPEBLVSDLORSSSEQAMRCSLITHEVEAFITTOVQOMYIGFLVPLAMS	240
Db	181	GSNIILATVLSIPEBLVSDLORSSSEQAMRCSLITHEVEAFITTOVQOMYIGFLVPLAMS	240
Qy	241	FCVLVIIRITLQARNERNKAIKVIIAVWVFIVFOLPYNGVLAOTVANFNITSTCEL	300
Db	241	FCVLVIIRITLQARNERNKAIKVIIAVWVFIVFOLPYNGVLAOTVANFNITSTCEL	300
Qy	301	SKOLNIAVDVTVSLACVRCVNPFLYAFIGVKFRNDIPKLFKDLGCLSQOLRQMSCRH	360
Db	301	SKOLNIAVDVTVSLACVRCVNPFLYAFIGVKFRNDIPKLFKDLGCLSQOLRQMSCRH	360
Qy	361	IRRSSMSVEAEITTTTSP	378
Db	361	IRRSSMSVEAEITTTTSP	378

```

RESULT 6
US-10-239-423-70
: Sequence 70. Application US/10239423
: Publication No. US2003018689A1
GENERAL INFORMATION:
APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERMANN, Knut;
APPLICANT: HETTLAND, Aleksandra; SPÖDERSER, Nikolaj
: TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
: TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
: TITLE OF INVENTION: for Treating Tumor Diseases and Inflammatory Diseases,
: TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
: TITLE OF INVENTION: Receptor Analytels and Chemokine Receptor/Ligand Interaction
: FILE REFERENCE: 022217us
: CURRENT APPLICATION NUMBER: US/10/239,423
: CURRENT FILING DATE: 2002-09-23
: PRIOR APPLICATION NUMBER: DE10015013.1
: PRIOR FILING DATE: 2000-03-31
: NUMBER OF SEQ ID NOS: 84
: SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 70

```

LENGTH: 378
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-70

Query Match 99.2%; Score 1907; DB 14; Length 378;
Best Local Similarity 99.2%; Pred. No. 4.6e-157;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLCKKQVRNPKAF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLCKKQVRNPKAF 60
QY 61 LPIMTSIIICFVGLGNGVLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFMAYSAAK 120
DB 61 LPIMTSIIICFVGLGNGVLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFMAYSAAK 120
QY 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
DB 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
QY 161 GSAILATVLSIPBELYSLOQRSSSQAMRCSLITHEVAFITIOVAQWVIGFLVPLAMS 240
DB 161 GSAILATVLSIPBELYSLOQRSSSQAMRCSLITHEVAFITIOVAQWVIGFLVPLAMS 240
QY 241 PCYLVIIIRTLQARNFERKAKIVIIAVVVVFIVQLPYNGVLAQTVAANFITSSTCEL 300
DB 241 PCYLVIIIRTLQARNFERKAKIVIIAVVVVFIVQLPYNGVLAQTVAANFITSSTCEL 300
QY 301 SKQLNIADVITYSLACVRCVNPFLYAFIVGKFRNDIFKLPDGLCSQEOQLRQMSSCRH 360
DB 301 SKQLNIADVITYSLACVRCVNPFLYAFIVGKFRNDIFKLPDGLCSQEOQLRQMSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

RESULT 7

US-10-435-696-48
Sequence 48, Application US/10435696
Publication No. US20040018525A1
GENERAL INFORMATION:
APPLICANT: Murtz, Ralph
APPLICANT: Munnes, Marc
APPLICANT: Kallabis, Harald
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
FILE REFERENCE: lea 36 108
CURRENT APPLICATION NUMBER: US/10/435,696
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: EP03003112.4
PRIOR FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: EP02010291.9
PRIOR FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 314
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-10-435-696-48

Query Match 99.2%; Score 1907; DB 15; Length 378;
Best Local Similarity 99.2%; Pred. No. 4.6e-157;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLCKKQVRNPKAF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLCKKQVRNPKAF 60

QY 61 LPIMTSIIICFVGLGNGVLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFMAYSAAK 120
DB 61 LPIMTSIIICFVGLGNGVLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFMAYSAAK 120
QY 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
DB 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
QY 161 GSAILATVLSIPBELYSLOQRSSSQAMRCSLITHEVAFITIOVAQWVIGFLVPLAMS 240
DB 161 GSAILATVLSIPBELYSLOQRSSSQAMRCSLITHEVAFITIOVAQWVIGFLVPLAMS 240
QY 241 PCYLVIIIRTLQARNFERKAKIVIIAVVVVFIVQLPYNGVLAQTVAANFITSSTCEL 300
DB 241 PCYLVIIIRTLQARNFERKAKIVIIAVVVVFIVQLPYNGVLAQTVAANFITSSTCEL 300
QY 301 SKQLNIADVITYSLACVRCVNPFLYAFIVGKFRNDIFKLPDGLCSQEOQLRQMSSCRH 360
DB 301 SKQLNIADVITYSLACVRCVNPFLYAFIVGKFRNDIFKLPDGLCSQEOQLRQMSSCRH 360
QY 361 IRRSSMSVEAETTTTFSP 378
DB 361 IRRSSMSVEAETTTTFSP 378

RESULT 8

US-10-251-385-204
Sequence 204, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Protein-Coupled
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO 204
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
US-10-251-385-204

Query Match 98.9%; Score 1900; DB 14; Length 378;
Best Local Similarity 98.9%; Pred. No. 1.9e-156;
Matches 374; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLCKKQVRNPKAF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDYIGNTTVDYTLFESLCKKQVRNPKAF 60
QY 61 LPIMTSIIICFVGLGNGVLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFMAYSAAK 120
DB 61 LPIMTSIIICFVGLGNGVLVLTYYIFKRLKTMTDYTLNLAVADILFLLTLPFMAYSAAK 120
QY 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
DB 121 SWPFGVHFCKLIIFAIYKMSFSGMILLICISIDRYVAIVQAVSARHRRARVLLISKLSCV 180
QY 161 GSAILATVLSIPBELYSLOQRSSSQAMRCSLITHEVAFITIOVAQWVIGFLVPLAMS 240
DB 161 GSAILATVLSIPBELYSLOQRSSSQAMRCSLITHEVAFITIOVAQWVIGFLVPLAMS 240
QY 241 PCYLVIIIRTLQARNFERKAKIVIIAVVVVFIVQLPYNGVLAQTVAANFITSSTCEL 300
DB 241 PCYLVIIIRTLQARNFERKAKIVIIAVVVVFIVQLPYNGVLAQTVAANFITSSTCEL 300

QY 301 SKOLNIAVDYVTSIACVRCNPNPLIYAFIVGVKFRNDIFKLFKDLGCLISQEOQLRQWSSCRH 360
DB 301 SKOLNIAVDYVTSIACVRCNPNPLIYAFIVGVKFRNDIFKLFKDLGCLISQEOQLRQWSSCRH 360
QY 361 IRRSSMSVEAETTTTSP 378
DB 361 IRRSSMSVEAETTTTSP 378

RESULT 9
US-10-425-114-56811

Sequence 56811, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 56811
LENGTH: 475
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4649-005-B4_F11.pap
US-10-425-114-56811

Query Match 94.4%; Score 1814; DB 15; Length 475;
Best Local Similarity 98.9%; Pred. No. 6.9e-149;
Matches 355; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 20 QVCLCODEVTDDYIGNTTVDYTLFESLSKQOVNFKAMFLPIMYSIICFVGLGNGLV 79
DB 117 KCLCDEVTDDYIGNTTVDYTLFESLSKQOVNFKAMFLPIMYSIICFVGLGNGLV 176
QY 80 VLTYYIFKRLKMTDTYLLNLAVADILFLTLPEMAYSAKSWVFGVHFKLIPAIYKMS 139
DB 177 VLTYYIFKRLKMTDTYLLNLAVADILFLTLPEMAYSAKSWVFGVHFKLIPAIYKMS 236
QY 140 FPSGMLLICISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELLISDL 199
DB 237 FPSGMLLICISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELLISDL 296
QY 200 ORSSSFQARCSLITEHVEAFITIOVAQWVIGFVPLMSPCYLVIIRTLQARRPERN 259
DB 297 ORSSSFQARCSLITEHVEAFITIOVAQWVIGFVPLMSPCYLVIIRTLQARRPERN 356
QY 260 KAIKVIIVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDYVTSIACVRC 319
DB 357 KAIKVIIVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDYVTSIACVRC 416
QY 320 CNPPLIYAFIVGVKFRNDIFKLFKDLGCLISQEOQLRQWSSCRHIRRSSMSVEAETTTTSP 378
DB 417 CNPPLIYAFIVGVKFRNDIFKLFKDLGCLISQEOQLRQWSSCRHIRRSSMSVEAETTTTSP 475

RESULT 10
US-09-903-377-2

Sequence 2, Application US/09903377
Patent No. US20020116727A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHEMOKINE
RECEPTOR 9A GENE DISRUPTIONS
FILE REFERENCE: R-365

QY 28 VDDYIGDMT-----VDYTLFESLSKQOVNFKAMFLPIMYSIICFVGLGNGLVLT 82
DB 1 MADDYSESTSSMEDYVNFETDFYCEKNNVQFASHFLPILTWLFIYVGLGNSLVTLV 60
QY 83 YIFKRLKMTDTYLLNLAVADILFLTLPEMAYSAKSWVFGVHFKLIPAIYKMSFPS 142
DB 61 YKCTRKVTMTDMFLNLAIADILFLTLPEMAYSAKSWVFGVHFKLIPAIYKMSFPS 120
QY 143 GMLLICISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELLISDLQRS 202
DB 121 CVLLIMCISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELLISDLQRS 180
QY 203 SSEQARCSLI-----TEHVEAFITIOVAQWVIGFVPLMSPCYLVIIRTLQARR 256
DB 181 SG-IAICTVVPDSDETKLSAIVLTKV---ILGFPLPVVWACCYTIITHTLQAKS 235
QY 257 ERNKAIVIAVAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIAVDYVTSIAC 316
DB 236 SKKAKATVITVLTAVVLSQFPNCLIVQITDAYAMFISNCAVSTNIDICPVOTQIAP 295
QY 317 VRCVNPPLIYAFIVGVKFRNDIFKLFKDLGCLISQEOQLRQWSSCRH---IRRSSMSVE 369
DB 296 FPCINPVLVYVGFGRFRDLVTLKMLGCLISQ---AQVVSFTRREGSKLSMLE 349

RESULT 11
US-09-952-385-2

Sequence 2, Application US/09952385
Patent No. US20020119504A1
GENERAL INFORMATION:
APPLICANT: Andrew, David P.
APPLICANT: Zabel, Brian A.
APPLICANT: Ponath, Paul D.
TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
FILE REFERENCE: IKS98-16
CURRENT APPLICATION NUMBER: US/09/952,385
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 09/266,464
PRIOR FILING DATE: 1999-03-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-09-952-385-2

Query Match 39.5%; Score 758.5; DB 9; Length 357;
Best Local Similarity 42.0%; Pred. No. 1.7e-57;
Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

```
QY 28 VTDYIGDNT-----VDYTLFESLCSKQDVNFKAMFLPIWYSIICFVGLGNGLVLT 82
DB 1 MADDYGESTSMEDYVNFNFTDFYCEKNNVROFASHFLPLWYLVFIYGAIGNSIVLIV 60
QY 83 YIFPRKLTMTDLYLNLAVADILFLTLTPMAVSAKSWGVGHFCKLIFAIYKMSFPS 142
DB 61 YWYCTRVKMTMDMFLNLAIADLFLVTLTPFWAIAAADQMKQTFMCKVNSMYKNFYS 120
QY 143 GMLLLCISIDRYVAIVQAVSAHRHARVLLSKLSCVSAIATVLSIPELLYSDLQRS 202
DB 121 CVLLIMCISVDRIYIAIAQAMRAHWREKRLYSKVCFTIWLVAALCIPELIYSQIKKE 180
QY 203 SSEQAMRCSLI-----TEHVEAFITIOVAQWVIGFLVPLAMSFCYLVITRTLOARNF 256
DB 181 SG--IAICTMVYPSDESTKLSAVLTKV---ILGFPLFPVWVACCYTIITHTLQAKKS 235
QY 257 ENRKAIXIIVAVVVFIVFQLPYNGVLAQTVANFNITSSTCELSKQNLIAVDVYSLAC 316
DB 236 SKHKLKVTITVLTIVFVLSQFPYNCILLVQITDAVAMFISNCVSTNIDICFOVTOTIAF 295
QY 317 VRCCVNPFLYAFIGYKFRNDIFKLFKDJGCSQEOBLRQWSSGRH---IRSSMSVE 369
DB 296 FHSCLNPLVYFVGFRFRDLVTKLKNLGCISQ---AQWVSFTRRREGSLKSSMLE 349
```

RESULT 12

```
US-09-966-755-2
/ Sequence 2, Application US/09966755
/ Publication No. US20030022238A1
/ GENERAL INFORMATION:
/ APPLICANT: Andrew, David P.
/ APPLICANT: Zabel, Brian A.
/ APPLICANT: Ponach, Paul D.
/ TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
/ FILE REFERENCE: LK989-16
/ CURRENT APPLICATION NUMBER: US/09/966,755
/ PRIOR FILING DATE: 2001-09-28
/ PRIOR APPLICATION NUMBER: US/09/266,464
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 357
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-966-755-2
```

Query Match 39.5%; Score 758.5; DB 10; Length 357;

Best Local Similarity 42.0%; Pred. No. 1.7e-57;

Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

```
QY 28 VTDYIGDNT-----VDYTLFESLCSKQDVNFKAMFLPIWYSIICFVGLGNGLVLT 82
DB 1 MADDYGESTSMEDYVNFNFTDFYCEKNNVROFASHFLPLWYLVFIYGAIGNSIVLIV 60
QY 83 YIFPRKLTMTDLYLNLAVADILFLTLTPMAVSAKSWGVGHFCKLIFAIYKMSFPS 142
DB 61 YWYCTRVKMTMDMFLNLAIADLFLVTLTPFWAIAAADQMKQTFMCKVNSMYKNFYS 120
QY 143 GMLLLCISIDRYVAIVQAVSAHRHARVLLSKLSCVSAIATVLSIPELLYSDLQRS 202
DB 121 CVLLIMCISVDRIYIAIAQAMRAHWREKRLYSKVCFTIWLVAALCIPELIYSQIKKE 180
QY 203 SSEQAMRCSLI-----TEHVEAFITIOVAQWVIGFLVPLAMSFCYLVITRTLOARNF 256
DB 181 SG--IAICTMVYPSDESTKLSAVLTKV---ILGFPLFPVWVACCYTIITHTLQAKKS 235
QY 257 ENRKAIXIIVAVVVFIVFQLPYNGVLAQTVANFNITSSTCELSKQNLIAVDVYSLAC 316
DB 236 SKHKLKVTITVLTIVFVLSQFPYNCILLVQITDAVAMFISNCVSTNIDICFOVTOTIAF 295
```

```
QY 317 VRCCVNPFLYAFIGYKFRNDIFKLFKDJGCSQEOBLRQWSSGRH---IRSSMSVE 369
DB 296 FHSCLNPLVYFVGFRFRDLVTKLKNLGCISQ---AQWVSFTRRREGSLKSSMLE 349
```

RESULT 13

```
US-10-000-759A-2
/ Sequence 2, Application US/10000759A
/ Publication No. US2002014191A1
/ GENERAL INFORMATION:
/ APPLICANT: Andrew, David P.
/ APPLICANT: Zabel, Brian A.
/ APPLICANT: Ponach, Paul D.
/ TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
/ FILE REFERENCE: 1855.1064-003
/ CURRENT APPLICATION NUMBER: US/10/000,759A
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: US/09/522,752
/ PRIOR FILING DATE: 2000-05-10
/ PRIOR APPLICATION NUMBER: US 09/266,464
/ PRIOR FILING DATE: 1999-03-11
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 357
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-000-759A-2
```

Query Match 39.5%; Score 758.5; DB 13; Length 357;

Best Local Similarity 42.0%; Pred. No. 1.7e-57;

Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

```
QY 28 VTDYIGDNT-----VDYTLFESLCSKQDVNFKAMFLPIWYSIICFVGLGNGLVLT 82
DB 1 MADDYGESTSMEDYVNFNFTDFYCEKNNVROFASHFLPLWYLVFIYGAIGNSIVLIV 60
QY 83 YIFPRKLTMTDLYLNLAVADILFLTLTPMAVSAKSWGVGHFCKLIFAIYKMSFPS 142
DB 61 YWYCTRVKMTMDMFLNLAIADLFLVTLTPFWAIAAADQMKQTFMCKVNSMYKNFYS 120
QY 143 GMLLLCISIDRYVAIVQAVSAHRHARVLLSKLSCVSAIATVLSIPELLYSDLQRS 202
DB 121 CVLLIMCISVDRIYIAIAQAMRAHWREKRLYSKVCFTIWLVAALCIPELIYSQIKKE 180
QY 203 SSEQAMRCSLI-----TEHVEAFITIOVAQWVIGFLVPLAMSFCYLVITRTLOARNF 256
DB 181 SG--IAICTMVYPSDESTKLSAVLTKV---ILGFPLFPVWVACCYTIITHTLQAKKS 235
QY 257 ENRKAIXIIVAVVVFIVFQLPYNGVLAQTVANFNITSSTCELSKQNLIAVDVYSLAC 316
DB 236 SKHKLKVTITVLTIVFVLSQFPYNCILLVQITDAVAMFISNCVSTNIDICFOVTOTIAF 295
QY 317 VRCCVNPFLYAFIGYKFRNDIFKLFKDJGCSQEOBLRQWSSGRH---IRSSMSVE 369
DB 296 FHSCLNPLVYFVGFRFRDLVTKLKNLGCISQ---AQWVSFTRRREGSLKSSMLE 349
```

RESULT 14

US-10-251-385-24

/ Sequence 24, Application US/10251385

/ Publication No. US20030105292A1

/ GENERAL INFORMATION:

/ APPLICANT: Behan, Dominic P.

/ APPLICANT: Liaw, Chen W.

/ TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G

/ TITLE OF INVENTION: Protein-Coupled

/ FILE REFERENCE: Recptors

/ CURRENT APPLICATION NUMBER: US/10/251,385

/ PRIOR FILING DATE: 2002-09-20

```

; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent version 3.1
; SEQ ID NO 24
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-251-385-24

```

```

Query Match      39.5%; Score 758.5; DB 14; Length 357;
Best Local Similarity 42.0%; Pred. No. 1.7e-57;
Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

```

```

Qy 28 VTDDYIGDNTT-----VDYTLFESLCSKDVNRKAFPLPIMYSIICFVGLGSLVLT 82
Db 1 MADDYGESTSSMEDYVNFPTDFYCEKNVRQASHFLPPLVLTIVTALGNSLIV 60

Qy 83 YIYFKRLKMTDTYLLNLAVADILFLTLTFPMVSAKSVFQVHFKCLIPAIYKMSFFS 142
Db 61 YMYCTRVKMTDMFLNLAIADLLFLVTLTFPMVIAADQMKFOTFMCKVNSMYKMFYS 120

Qy 143 GMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELYSDLQRS 202
Db 121 CVLLIMCISIDRYVIALAQANRAHTWREKRLYSKMCFTIWLVAALCIPILYSQKEE 180

Qy 203 SSEQARCSLI-----TEHVEAFITIOVQAVNIGFLVPLPILAMSPCYLVIIRTLQARNF 256
Db 181 SG--IAICTVNVPSDESTYKLSAVLTIKV---ILGFPLPVVMAACCTYIIHTLIQAKS 235

Qy 257 ERNKAIVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIADVTYSLAC 316
Db 236 SKKALKVITITVLTFLVLSQFPYNCILVQTIADAVAMFISNCAVSTNIDICFOVTOTIAR 295

Qy 317 VRCCVNPFLYAFIGVKFRNDIFKLFDLGLCSQEQOLQWSSCRH---IRSSMSVE 369
Db 296 FHSCLNPVLVYFVGERFRRLDVLTCLKNLGCTISQ---AQWVSFTRRBSGLKLSMLLE 349

```

```

RESULT 15
US-10-225-567A-241
; Sequence 241, Application US/10225567A
; Publication No. US2003013798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burnet, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: Patent version 3.1
; SEQ ID NO 241
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-241

```

```

Query Match      39.5%; Score 758.5; DB 14; Length 357;
Best Local Similarity 42.0%; Pred. No. 1.7e-57;
Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

```

```

Qy 28 VTDDYIGDNTT-----VDYTLFESLCSKDVNRKAFPLPIMYSIICFVGLGSLVLT 82
Db 1 MADDYGESTSSMEDYVNFPTDFYCEKNVRQASHFLPPLVLTIVTALGNSLIV 60

Qy 83 YIYFKRLKMTDTYLLNLAVADILFLTLTFPMVSAKSVFQVHFKCLIPAIYKMSFFS 142
Db 61 YMYCTRVKMTDMFLNLAIADLLFLVTLTFPMVIAADQMKFOTFMCKVNSMYKMFYS 120

```

```

Qy 143 GMLLLCISIDRYVAIVQAVSAHRHARVLLISKLSVGSAILATVLSIPELYSDLQRS 202
Db 121 CVLLIMCISIDRYVIALAQANRAHTWREKRLYSKMCFTIWLVAALCIPILYSQKEE 180

Qy 203 SSEQARCSLI-----TEHVEAFITIOVQAVNIGFLVPLPILAMSPCYLVIIRTLQARNF 256
Db 181 SG--IAICTVNVPSDESTYKLSAVLTIKV---ILGFPLPVVMAACCTYIIHTLIQAKS 235

Qy 257 ERNKAIVIIAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIADVTYSLAC 316
Db 236 SKKALKVITITVLTFLVLSQFPYNCILVQTIADAVAMFISNCAVSTNIDICFOVTOTIAR 295

Qy 317 VRCCVNPFLYAFIGVKFRNDIFKLFDLGLCSQEQOLQWSSCRH---IRSSMSVE 369
Db 296 FHSCLNPVLVYFVGERFRRLDVLTCLKNLGCTISQ---AQWVSFTRRBSGLKLSMLLE 349

```

Search completed: February 25, 2005, 02:35:30
Job time: 136 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2005, 02:14:37 ; Search time 40 Seconds
(without alignments)
909,248 Million cell updates/sec

Title: US-10-749-990-2

Sequence: 1 MDLGRPKMSVLLVALLVIFQ.....RHRRSSMSVEAEITTTTSP 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1922	100.0	378	2	A45680 G protein-coupled
2	1907	99.2	378	2	B55735 lymphocyte-specific
3	1696	88.2	378	2	A55735 G protein-coupled
4	707.5	36.8	369	2	JC5068 G protein-coupled
5	618	32.2	350	2	JN0621 G protein-coupled
6	614	31.9	360	2	A57160 chemokine (C-C) re
7	595	31.0	360	2	JC4587 chemokine (C-C) re
8	574	29.9	327	2	S5162 MDCR15 protein - h
9	574	29.9	358	2	A53752 Interleukin-8 rece
10	574	29.9	372	2	S26667 G protein-coupled
11	570.5	29.7	367	2	JE0349 Interferon-gamma
12	570	29.7	374	2	J18450 chemokine (C-C) re
13	567.5	29.5	360	2	JC2443 chemokine (C-C) re
14	565	29.3	355	2	JQ1231 Interleukin-8 rece
15	562.5	29.3	374	2	S42628 G protein-coupled
16	561.5	29.2	360	2	A53611 Interleukin-8 rece
17	556.5	29.0	374	2	S32785 G protein-coupled
18	553.5	28.8	355	2	A45177 chemokine (C-C) re
19	553	28.8	352	2	A43113 chemokine (C-C) re
20	549.5	28.6	353	2	S28787 neuropeptide Y/pep
21	539	28.0	359	2	A48921 Interleukin-8 rece
22	538	28.0	352	2	A45747 neuropeptide Y/pep
23	533	27.7	350	2	A39445 Interleukin-8 rece
24	530.5	27.6	356	2	S42096 Interleukin-8 rece
25	529	27.5	359	2	A49341 MIP-1 alpha recept
26	525	27.3	352	2	G00048 fusin (FUSIN) - C
27	524.5	27.3	355	2	G02436 chemokine (C-C) re
28	524.5	27.3	383	2	S55594 G protein-coupled
29	522	27.2	354	2	B55733 G protein-coupled

30	509.5	26.5	355	2	I49339 macrophage infla
31	500	26.0	355	2	JC5067 G protein-coupled
32	482.5	25.1	355	2	JC4304 orphan G protein-c
33	478.5	24.9	356	2	I49340 MIP-1 alpha recept
34	477.5	24.8	354	2	A23669 Interleukin-8 rece
35	477	24.8	354	2	I58186 probable G protein
36	441.5	23.0	362	2	JN0694 angiotensin II rec
37	434	22.6	359	2	S15403 angiotensin II rec
38	433.5	22.6	359	2	A42656 angiotensin II rec
39	433	22.5	359	2	S44425 angiotensin II rec
40	430	22.4	359	2	JC1104 angiotensin II rec
41	429	22.3	359	2	JC2134 angiotensin II rec
42	428	22.3	359	2	JC1194 angiotensin II rec
43	426.5	22.1	359	2	JQ1516 angiotensin II rec
44	424	22.1	359	2	A48857 angiotensin II rec
45	423	22.0	359	2	JH0621 angiotensin II rec

ALIGNMENTS

RESULT 1

A45680 G protein-coupled peptide receptor EBI 1 - human

C/Species: Homo sapiens (man)

C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A45680

R/Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.

J. Virol. 67, 2209-2220, 1993

U./Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p

A/Reference number: A45680; MID:93188173; PMID:8383238

A/Accession: A45680

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-378 <R>

A/Cross-references: UNIPROT:P32248; GB:I08176; NID:G183484; PID:G183485

A/Experimental source: B-lymphocytes

A/Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBI:P.127095)

C/Superfamily: vertebrate rhodopsin

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match	100.0%	Score 1922	DB 2	Length 378
Best Local Similarity	100.0%	Pred. No. 8e-153		
Matches 378	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MDLGRPKMSVLLVALLVIFQVCLCDBVTDDYIGDNTVDYTLFESLCSKQDVRNFRAMP	60	
DB	1	MDLGRPKMSVLLVALLVIFQVCLCDBVTDDYIGDNTVDYTLFESLCSKQDVRNFRAMP	60	
QY	61	LPIMYSIICFVGILGNGLVLTFTYFKRLKTMVDTYLAALAVADILFLTLPRMAYSAK	120	
DB	61	LPIMYSIICFVGILGNGLVLTFTYFKRLKTMVDTYLAALAVADILFLTLPRMAYSAK	120	
QY	121	SWFVGVPCKLIPAIYKMSFSGMLLLCTSIDRYVAIVQASARHRRARVLLISKLSCV	180	
DB	121	SWFVGVPCKLIPAIYKMSFSGMLLLCTSIDRYVAIVQASARHRRARVLLISKLSCV	180	
QY	181	GSNIIATVLSIPBLAYSDIQRSSSQAMRCSLITHEVEAFITTVQAVMAYIGFVPLLAWS	240	
DB	181	GSNIIATVLSIPBLAYSDIQRSSSQAMRCSLITHEVEAFITTVQAVMAYIGFVPLLAWS	240	
QY	241	FCVLIIRTLQARNFERKAIKVIIVAVVFIFQLPNGVLAQTAVNFINITSSTCEL	300	
DB	241	FCVLIIRTLQARNFERKAIKVIIVAVVFIFQLPNGVLAQTAVNFINITSSTCEL	300	
QY	301	SKQLNIAVDVYSLACVRCVNPFLVAFIGVFRNDIFKLFDLGLCSQDQLRQSSCRH	360	
DB	301	SKQLNIAVDVYSLACVRCVNPFLVAFIGVFRNDIFKLFDLGLCSQDQLRQSSCRH	360	
QY	361	IRRSSMSVEAEITTTTSP 378		
DB	361	IRRSSMSVEAEITTTTSP 378		

```
RESULT 2
B55735
Lymphocyte-specific G protein-coupled receptor EB11 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: B55735; S52443
R:Schweickart, V.L.; Raport, C.U.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835; PMID:7851893
A:Accession: B55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: UNIPROT:P32248; GB:L31581; NID:9468319; PIDN:AAA74231.1; PID:9468320
R:Burschtaler, R.; Kempkes, B.; Staube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically trans
A:Reference number: S52443
A:Accession: S52443
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 21-378 <BUR>
A:Cross-references: EMBL:X84702
C:Genetics:
A:Gene: GDB:CMKBR7; EB11; BLR2; CCR7
A:Cross-references: GDB:342065; OMIM:600242
A:Superfamily: 17q12-17q21.2
C:Keywords: G protein-coupled receptor

Query Match          99.2%; Score 1907; DB 2; Length 378;
Best Local Similarity 99.2%; Pred. No. 1.4e-151;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLTFESLCSKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLTFESLCSKQVRNFKAMF 60
QY 61 LPIMYSIIICFVGLGNGVLLVITYYFKRLKMTDPTYLNLAVADILFLITLPPMAVSAK 120
DB 61 LPIMYSIIICFVGLGNGVLLVITYYFKRLKMTDPTYLNLAVADILFLITLPPMAVSAK 120
QY 121 SWVPGVHFCCKLIFALYKMSFSGMILLICISIDRYVAIVQASRRHRARVLLISKLSKV 180
DB 121 SWVPGVHFCCKLIFALYKMSFSGMILLICISIDRYVAIVQASRRHRARVLLISKLSKV 180
QY 181 GSAILATVLSIPELLYSDLQSSSEQAMRCSLITEHVEAFITIQVAQWVIGFLVPLAMS 240
DB 181 GSAILATVLSIPELLYSDLQSSSEQAMRCSLITEHVEAFITIQVAQWVIGFLVPLAMS 240
QY 241 FCYLVITRTLLQARNPERKAIKVIIAVVVFVFPQLPNGVLAQTVAENFNTSSTCEL 300
DB 241 FCYLVITRTLLQARNPERKAIKVIIAVVVFVFPQLPNGVLAQTVAENFNTSSTCEL 300
QY 301 SKQLNIADVTVSLACVCCVNPFLYAFGVKFRNDIFKLPDGLCSOEOLROMSSCRH 360
DB 301 SKQLNIADVTVSLACVCCVNPFLYAFGVKFRNDIFKLPDGLCSOEOLROMSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378

RESULT 3
A55735
G protein-coupled receptor EB11 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C:Accession: A55735
R:Schweickart, V.L.; Raport, C.U.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
```

```
Genomics 23, 643-650, 1994
A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor
A:Reference number: A55735; MUID:95154835; PMID:7851893
A:Accession: A55735
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-378 <SCH>
A:Cross-references: UNIPROT:P47774; GB:L31580; NID:9468340; PIDN:AAA74232.1; PID:9468341
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match          88.2%; Score 1696; DB 2; Length 378;
Best Local Similarity 86.0%; Pred. No. 5.7e-134;
Matches 325; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLTFESLCSKQVRNFKAMF 60
DB 1 MDLGRPKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDYLTFESLCSKQVRNFKAMF 60
QY 61 LPIMYSIIICFVGLGNGVLLVITYYFKRLKMTDPTYLNLAVADILFLITLPPMAVSAK 120
DB 61 LPIMYSIIICFVGLGNGVLLVITYYFKRLKMTDPTYLNLAVADILFLITLPPMAVSAK 120
QY 121 SWVPGVHFCCKLIFALYKMSFSGMILLICISIDRYVAIVQASRRHRARVLLISKLSKV 180
DB 121 SWVPGVHFCCKLIFALYKMSFSGMILLICISIDRYVAIVQASRRHRARVLLISKLSKV 180
QY 181 GSAILATVLSIPELLYSDLQSSSEQAMRCSLITEHVEAFITIQVAQWVIGFLVPLAMS 240
DB 181 GSAILATVLSIPELLYSDLQSSSEQAMRCSLITEHVEAFITIQVAQWVIGFLVPLAMS 240
QY 241 FCYLVITRTLLQARNPERKAIKVIIAVVVFVFPQLPNGVLAQTVAENFNTSSTCEL 300
DB 241 FCYLVITRTLLQARNPERKAIKVIIAVVVFVFPQLPNGVLAQTVAENFNTSSTCEL 300
QY 301 SKQLNIADVTVSLACVCCVNPFLYAFGVKFRNDIFKLPDGLCSOEOLROMSSCRH 360
DB 301 SKQLNIADVTVSLACVCCVNPFLYAFGVKFRNDIFKLPDGLCSOEOLROMSSCRH 360
QY 361 IRRSSMSVEAETTTTFFSP 378
DB 361 IRRSSMSVEAETTTTFFSP 378

RESULT 4
JCS068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JCS068
R:Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like ge
A:Reference number: JCS067; MUID:97040707; PMID:8886020
A:Accession: JCS068
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:Cross-references: EMBL:Z79784; NID:91668737; PIDN:CA802144.1; PID:91668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-C14
A:Cross-references: GDB:5370639; OMIM:601835
A:Map position: 6q27-6q27
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>
```

[illegible]

```

RESULT 5
JN0621
G-protein-coupled receptor type B - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C/Accession: JN0621
R/Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993
A>Title: Identification of novel members of G-protein coupled receptor superfamily expre
A/Reference number: JN0621; MUID:93326166; PMID:8392843
A/Accession: JN0621
A/Molecule type: mRNA
A/Residues: 1-350 <MAN>
A/Cross-references: UNIPROT:P35350; GB:S63846; NID:g399710; PIDN:AAB27547.1; PID:g399711147.1;
A/Experimental source: tongue taste papillae
C/Comment: This protein is involved in modulating taste sensitivity or regeneration of t
C/Superfamily: vertebrate rhodopsin
C/keywords: G-protein-coupled receptor; glycoprotein; receptor; transmembrane protein
F/42-66/Domains: transmembrane #status predicted <TM1>
F/80-99/Domains: transmembrane #status predicted <TM2>
F/114-135/Domains: transmembrane #status predicted <TM3>
F/154-175/Domains: transmembrane #status predicted <TM4>
F/200-222/Domains: transmembrane #status predicted <TM5>
F/247-265/Domains: transmembrane #status predicted <TM6>
F/284-306/Domains: transmembrane #status predicted <TM7>
F/6.19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          32.2%; Score 618; DB 2; Length 350;
Best Local Similarity 36.8%; Pred. No. 4.5e+44;
Matches 135; Conservative 70; Mismatches 124; Indels 38; Gaps 8;

Oy DEWDVDYDGD---NTTVDTLFEELSCSKDVDRNFAMVLPIMYSILICVGVLGGGLVTLT 82
Db   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 6 NOSDYVEEEMANDTHYSQIEVALCIKEBKRKAKFLPEPFTTAFITIGLAGNSTVAI 65
Db   :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 83 YIFGRRLKTMTDTYLNLAVADILFLTLTPWASAAKSWWGVHPCULPAIRIKMSFFS 142
Db   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 66 YAAYKKRTKTDVVYILNALVADLFLLPLPMANVANAHGMVLGKMKCVTSALTYVNFS 125
Db   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 143 GMILLLCISDIRVAIVQAVSAHRBRARVULLSTLSCGSNAILATVISLEPLLSDLDORS 202
Db   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 126 GMQFLACISTDIRRYMYATAPSS---QSQSGVKRPCHWICGCWVAAILSLSPQLVFPTYNHK 181
Db   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 203 SSQQAMRC-SLITEHVEAF--TIQAQMVIQFLVPLLAWSFCYLVIIRTLQARNPERN 259

```

[illegible]

RESULT 6

A57160
chemokine (C-C) receptor 4 - human
N/Alternate names: C-C CKR-4
C/Species: Homo sapiens (man)
C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #ext_change 09-Jul-2004
C/Acessionion: A57160
R/Power: C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Weisberg, E.H.
J./BIOL. Chem. 270, 19495-19500, 1995
A>Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA
A/Reference number: A57160; MUID:95370289; PMID:7642634
A/Accession: A57160
A>Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-360 <POW>
A/Cross-references: UNIPROT:P51679; GB:X85740; NID:g1370103; PIDN:CAAS9743.1; PID:g9711455
A/Note: source clone KS-5
C/Genetics:
A/Gene: GDB:CMKR4
A/Cross-references: GDB:677463
A/Map position: 3p21-3p21
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protease
F/40-65/Domain: transmembrane #status predicted <TM1>
F/76-97/Domain: transmembrane #status predicted <TM2>
F/112-133/Domain: transmembrane #status predicted <TM3>
F/151-175/Domain: transmembrane #status predicted <TM4>
F/208-226/Domain: transmembrane #status predicted <TM5>
F/243-264/Domain: transmembrane #status predicted <TM6>
F/291-308/Domain: transmembrane #status predicted <TM7>
F/329-350/Domain: disulfide bonds: #status predicted
F/329-350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
F/145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F/183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 31.9%; Score 614; DB 2; Length 360;
Beat Local Similarity 39.3%; Pred. No. 16-43;
Matches 126; Conservative 75; Mismatches 110; Indels 10; Gaps 5;

OY 27 EVTDYIGDNTVDVDTLEPSL---CSKDVRFKMFLLIMYSIICFGVLGNGLVLTLY 83
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 5 DIADTLDSEISYNYYLVESIPKCPCKEGRKAFGEFLPLPVSIVVFGLGNSVVALL 64
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 84 IYFKLKMTDPTVYLNLAVADILFTLPFMAYSAKSANVFGVHFCFLIFAIYKMSFPSSG 143
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 65 FKYRLRSMTDPVYLNLAISDLFLVPSPDFPKGVYADDQVFGGLCKMISMNVLVGFSG 124
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 144 MLLLCISIDRYVAIVQAASHRRARVLLISKSCVGSAILATVLSIPELLYSD--LQR 201
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 125 IPFWALMSIDRIALIVHAFS--LRARTLTGVITSLAMSVAVFASLPGLFSTCYTER 182
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 202 SSSDAQMSLITEVEAFITIOVQOMVIGFVPLLMASFVVIIRTLIQANPERNKRA 261
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 183 NHYICKTKYSLNSTTWKULSSLIET--NIIGLVIPAGIMLFCTSMIRITLOHCNKKKA 240
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 262 IKVIAVVVFVIFQLPYNGVLLAQTVANFNITTSCTBLSKOLNIAYDVITYASVCRCV 321

Db 241 VAMIAVAVVVLFGFTPTNIVFLFETLVELEVLQD-CTFERLYDAIQATETLAFVHCL 299
Qy 322 NPLVYAFGVKFRNDIFKLFK 342
Db 300 NPITYFLGEKFRKYLQLFK 320

RESULT 7
JC4587
chemokine (C-C) receptor 4 - mouse
C.Species: Mus musculus (house mouse)
C.Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C.Accession: J04587
R.Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A.Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
A.Reference number: J04587; MUID:96136324; PMID:8573157
A.Accession: J04587
A.Molecule type: mRNA
A.Residues: 1-360 <HOO>
A.Cross-references: UNIPROT:P51680; EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g116
A.Experimental source: thymus
C.Genetics:
A.Gene: cc ckr-4
C.Superfamily: vertebrate rhodopsin
C.Keywords: glycoprotein; phosphoprotein; receptor; thymus
F.2,183,194/Binding site: carboxydrate (Asn) (covalent) #status predicted
F.72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
F.145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F.321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 31.0%; Score 595; DB 2; Length 360;
Best Local Similarity 35.9%; Pred. No. 3.9e-42;
Matches 133; Conservative 72; Mismatches 121; Indels 44; Gaps 8;

Qy 27 EYTDYIGNTVDYDTPESL---CSKQDVRFKAMFLPIMYSIICFVGLNGLVLT 83
Db 5 EYTDYDQETVNSYFVSESMKPCFKEGIKAFGEVFLPPLSLVFLGLFGNSVVVL 64

Qy 84 IYFKRLKMTDTYLLNLAVADILFLTPFMAYSAKSWPVGHFCKLFAIYKMSFSG 143
Db 65 FRYKRLKMTDYLLNLASDLFLTPFMSLPFGVYAADQVFLGCKIYSMYLVGFYSG 124

Qy 144 MLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCVGSALITVLSIPELLYSDFSS 203
Db 125 IFFIMMSIDRYLAIVHAVFS--LKARLTLYGVITSLTWSVAVFASLPGLFS----- 176

Qy 204 SQQARCSLITHEVAFTIYQAQ-----MIGFLVPLAMSFCYVITRL 250
Db 177 -----TCYTEHNHTYCKTQYSVNSTWKLSSLEINVLGLIPGLMFWYSMIRTL 229

Qy 251 LQARNFERKAIKIVIAVVVPIVFPOLPYNGLVQTVANFITSCTELSKQNLAVDV 310
Db 230 QICKKEKRRARVIMFGVVVFLGFTPTNIVFLFETLVELEVLQD-CTLEKLYDAIQA 288

Qy 311 TVSLACVRCVNPFLYAFIVGVKFRNDIFLKFQDGLSGEOELRWSSCRH-----IRSS 365
Db 289 TETLAFIHCCINPVIYFVFGKFRKYLQLFK--CRGPLV-----CGHCPFLQYASD 341

Qy 366 MSVEAETTT 375
Db 342 MSSSYTOST 351

RESULT 8
S56162
MDCR15 protein - human
C.Species: Homo sapiens (man)
C.Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C.Accession: S56162
R.Bareille, L.; Loeschner, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995

A>Title: Sequence variation of a novel heptahelical leucocyte receptor through alternati
A.Reference number: S56162; MUID:95366951; PMID:763692
A.Accession: S56162
A.Status: preliminary; nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-327 <BAR>
A.Cross-references: EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784
C.Superfamily: vertebrate rhodopsin

Query Match 29.9%; Score 574; DB 2; Length 327;
Best Local Similarity 36.7%; Pred. No. 2e-40;
Matches 122; Conservative 74; Mismatches 118; Indels 18; Gaps 7;

Qy 55 NFKAMFLPIMYSIICFVGLNGLVLTYYIFKRLKMTDTYLLNLAVADILFLTPFW 114
Db 3 SFKAFVHVAVASLIPFLGVIGVNLVILERHQRTSSTETPLFHLAVADILVFLPFA 62

Qy 115 AVSAKSWPVGHFCKLFAIYKMSFSGMLLCISIDRYVAIVQAVSAHRHRAVLLI 174
Db 63 VAEKSGVNLGTFCLKTYIALHKVFCSSLLACLADRYAIVAAVAAHRH--LLS 120

Qy 175 SKLSCVGSALITVLSIPELLYSDFQSSSEQAM-RCSLITEH--VEAFTIYQAQVYI 230
Db 121 IHTCGTIWVGFLLALPEILFAKYSQGHNNNSLPRCTFSGENQAEHTAMFTSRFLYHA 180

Qy 221 GFVLPLAMSCYLVITITLQA-RNFERKAIKIVIAVVVPIVFPOLPYNGLVLAQVYA 289
Db 181 GFLPLMLVMGCVGVVHRLRQARRPOROKAVRAIVLTSIFFLCWSYHIVIFLDITLA 240

Qy 220 NFNITSTCELSKQNLINVDYVLSACRCCNPFLYAFIVGVKFRNDIFKLFKDCLSQ 349
Db 241 RIKAVDNTCKLNGSLPVAITMCEFLGLAHCCNPLVIFAGVKRSRLTLTKLGCTSP 300

Qy 350 EQLRQ----WSSCRHIRSSMSVEAETTTTFS 377
Db 301 ASLQCLFPW-----RRSLSS-ESENATSLT 325

RESULT 9
A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C.Accession: A53752
R.Pirado, G.N.; Thomas, K.M.; Suzuki, H.; Larosa, G.J.; Wilkinson, N.; Folco, E.; Navarro, J.
J. Biol. Chem. 269, 12391-12394, 1994
A.Title: Molecular characterization of a novel rabbit interleukin-8 receptor isoform.
A.Reference number: A53752; MUID:94230294; PMID:8175642
A.Accession: A53752
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-358 <PRA>
A.Cross-references: UNIPROT:P35344; GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.9%; Score 574; DB 2; Length 358;
Best Local Similarity 33.8%; Pred. No. 2.2e-40;
Matches 125; Conservative 74; Mismatches 123; Indels 48; Gaps 6;

Qy 30 DDYIDGNTVDY-----TLFESLCSKQDVRFKAMFLPIMYSIICFVGLNGLVLT 83
Db 12 EDFGDFSNYSYSTDLPPTLDSAPCRSESLSTNSVYVLIYIIVFLSLGNSLVMVLI 71

Qy 84 IYFKRLKMTDTYLLNLAVADILFLTPFMAYSAKSWPVGHFCKLFAIYKMSFSG 143
Db 72 LYSRSTCVTDYLLNLAIADILFLTPPIPMASRVHGTETPLCKVVSIVKENVFSG 131

Qy 144 MLLLCISIDRYVAIVQAVSAHRHRAVLL--ISKLSVGSALITVLSIPELL----- 195
Db 132 ILLALCISVDRLAIV-----HATRMIGQRHVLKFCISMWGVSLISLPILLFRVA 184

Qy 196 -----YSDLRSSSEQAMRCSLITHEVAFTIYQAQVIMIGFLVPLAMSCYLV 245

```

Db      185 ITPPNSSPVCYEDMGKSTAKMRY-----VLRLLPOTFGTILPMLCYVF 231
Qy      246 IIRTLQANFNENKAIKYIIAVVVFIVFQLPNGVLAQTAVANNTISSTELSKOLN 305
Db      232 TLRTLQANMGQHRMRYIFAVVLLFLCMLPYNVLVLTDLTMRHVIGTERANDID 291
Qy      306 IAYDVTYSLACRCCNPFVYAFVGVKFNNDIFKLPDGLCSQEOQLRQMSCRHTRRS 365
Db      292 RALDAEIIIGPLHSCINPIYAFVIGQFRYGLKILIAHGLISKEFLAKESRPSFVASS 351
Qy      366 MSVEAETTT 375
Db      352 ----GNTSTT 357

RESULT 10
S26667
G:protein-coupled receptor BLR1 - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S26667
R:Doberer, T.; Wolf, I.; Emrich, T.; Liipp, M.
Eur. J. Immunol. 22, 2795-2799, 1992
A:Title: Differentiation-specific expression of a novel G protein-coupled receptor from
A:Reference number: S26667; MUID:93049615; PMID:1425907
A:Accession: S26667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-372 <DOB>
A:Cross-references: UNIPROT:P32302; EMBL:X68149; NID:g29459; PIDN:CAA48252.1; PID:g29460
C:Genetics:
A:Gene: GDB:BLR1
A:Cross-references: GDB:136235; OMIM:601613
A:Map position: 15q26.1-15q26.1
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      29.9%; Score 574; DB 2; Length 372;
Best Local Similarity 35.9%; Pred. No. 2,3e-40;
Matches 126; Conservative 78; Mismatches 125; Indels 22; Gaps 9;

Qy      40 DYTLES-LCSKD--VNFKAMFLPIMYSICFVGLGNGLVLTYYFKLKTMTDT 95
Db      29 DTSLVENHLCPTAEGELMASFKAVFVPVAVSLFLGLVIGNVLVLTLEHRQTRSTET 88
Qy      96 YLLNLAVALDILFLTPMAVSAKSMVGVNHCXLIIFAYKMSFSGMILLICISIDRY 155
Db      89 FLPHLAVADLLVFLIPFAVAGSVGVWLTGLCKTVIALHKVNFYCSSLACIADVRY 148
Qy      156 VAIVQAVSHRRARVLLISKSCVSAIATVLSIPELLYSDLQSSSQAM-RCSLIT 214
Db      149 LAIVAVHVRHRR--LISHTICGIIWVGLLALPEILFAYVSGHHNSLPKCTFSG 206
Qy      215 EH--VEAFITIQAVOMVIGFLVPLLMASFCYLVIRTLQA-RNFERKAIKVIIAVV 270
Db      207 ENQAEHTAMFTSRFLYHVAAGFLPMLVMGVCYGVVHRLQAQRROQGAVALILYS 266
Qy      271 VFIVPOLPNGVLAQTAVANNTISSTELSKOLNAYDVTYSLACRCCNPFVYAFV 330
Db      267 IFPLCWSPHIVIFLDTLRLAKAVDTCKLNGSLPALIMCEPLGLAHCCINMLTTFVG 326
Qy      331 VFERNDFPKLPKDLGCLSQEOQLRQ----WSSCHIRRSSMSVAETTTFS 377
Db      327 VFRRSLSKLLTLCGCTGPASLCQLFPPSW-----RRSLS-ESENATSLT 370

RESULT 11
JEO349
interferon-inducible protein 10 (IP-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C:Accession: JEO349

```

```

R:Tamatu, M.; Tomiaga, Y.; Yatsunami, K.; Natumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
A:Reference number: JEO349; MUID:99009219; PMID:9790904
A:Accession: JEO349
A:Molecule type: mRNA
A:Residues: 1-367 <TM>
A:Cross-references: UNIPROT:Q9QW06; DDBJ:AB03174; NID:g3798731; PIDN:BA34045.1; PID:g3;
C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C:Superfamily: vertebrate rhodopsin

```

```

Query Match      29.7%; Score 570.5; DB 2; Length 367;
Best Local Similarity 37.0%; Pred. No. 4,3e-40;
Matches 130; Conservative 63; Mismatches 141; Indels 17; Gaps 6;

Qy      32 YIGDNTVDYTLFES-----LCSKDVRFKAMFLPIMYSICFVGLGNGLVLTYY 83
Db      18 FLEENSTPYDGENSDSPDPCQDPSLAFDRFLLALYSILFLDLGNGVAAVLY 77
Qy      84 IYFKRLKTMTDYLLNLAVALDILFLTPFMAVSAKSMVGVNHCXLIIFAYKMSFSEG 143
Db      78 LSGRTALSTDFELHLAVADVLTFLTPMAVDAVQVFGGLCKVAGALFNINFYAG 137
Qy      144 MLLLCISTDRYVAIYQAVSHRRARVLLISKSCVSAIATVLSIPELLYSDLQSS 203
Db      138 AFLALCISDFRYSIHAHQIIRDRPRV--ALTCIVMGCLLPALDPFYLSDYQ 195
Qy      204 SEQAMRCSLITHEVAFTITQAVOMVIGFLVPLLMASFCYLVIRTLQANFERKAIK 263
Db      196 RLAKATGQYNPROV-GRTLYRLVQLVAGFLPLVMAVYCYAHILANVLVSRGRRFRA 254
Qy      264 VVIAVVVEIVPOLPNGVLAQTAVANNTISSTELSKOLNAYDVTYSLACRCCNVP 323
Db      255 LVVVVVAAPVACWTPFHLVLDLMDVGLARNGRSHSVAKSVTSGMGYHCCCLNP 314
Qy      324 FIYAFVGVKFNNDIFKLPDGLCSQEOQLRQMSCRHTRRSMSVAETTT 373
Db      315 LLYAFVGVKFNNDIFKLPDGLCSQEOQLRQMSCRHTRRSMSVAETTT 360

RESULT 12
I38450
chemokine (C-C) receptor 2, splice form A - human
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C:Accession: I38450
R:Chato, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant prot
A:Reference number: A53477; MUID:94195821; PMID:8146186
A:Accession: I38450
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RES>
A:Cross-references: UNIPROT:P41597; EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g4725;
C:Genetics:
A:Gene: GDB:CMKBR2
A:Cross-references: GDB:337364; OMIM:601267
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane
F:44-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:208-226/Domain: transmembrane #status predicted <TM5>
F:244-265/Domain: transmembrane #status predicted <TM6>
F:292-309/Domain: transmembrane #status predicted <TM7>
F:14-binding site: carbohydrate bonds: #status predicted
F:32-277,113-190/Disulfide bonds: #status predicted

```

```

Query Match      29.7%; Score 570; DB 2; Length 374;

```

Best Local Similarity 39.6%; Pred. No. 4.9e-40; Matches 128; Conservative 65; Mismatches 110; Indels 20; Gaps 10;

QY 26 DEVTDDYIGDNTTVDYTLTPESSLSCKDVNFRAMFLPIMYSIICFVGLGNGLVLTYY 85
18 EVVT-----TFPYD-YGAPCHKFDVQIGAQLLPPLYSVPIFGFGNMLVVLILIN 69

QY 86 FRKLKMTDTYLLNLAADVILFLTLTPFAVYSAKSWFGVHFCKLIPAIYKMSFSGML 145
70 CKKLKCLTDIYLLNLAISDLFLTLPLMAHSAANEMVFGNAMCKLFTGLYHIGVGGIF 129

QY 146 LILCISIDRYVAIYQAVSAHRRARVLLISKLSGSAIILATVLSIPELLYSDLRSSSE 205
130 FILLITIDRYLAIYVAHVA--LKARTVFGVTSVITWLVAVPASVPGIIFPKCKQEDSV 187

QY 206 QAMRCS-LITEHVEAFITIQVQWVIGFVPLPLMSFCYLVIRTLQARN-FERNKAIR 263
188 YV--CGPYPRGMNPHITM--RNILGLVLPPLIIVICSGILKTLRCRNEKSHRAVR 243

QY 264 VTIAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIADYVTSIACVRCVNP 323
244 VIPTIMIVFLEFMPYNYIILNTFOEF-FGLSNCESTSQLDAQVETLGMTHCCINP 302

QY 324 FLVAFIVGKERNDIFKLFK 346
303 IIVAFVGEKFRYSVFFR 322

Db

RESULT 13
JG2443
chemokine (C-C) receptor 2, splice form B - human
N/Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chem
C/Species: Homo sapiens (man)
C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C/Accession: JG2443; 138463
A/Accession: JG2443
A/Molecule type: mRNA
A/Residues: 1-360 <YAM>
A/Cross-references: UNIPROT:P41597; DDBJ:D299984; NID:G531246; PIDN:BA06253.1; PID:G5312
R/Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
A/Title: Molecular cloning and functional expression of a human monocyte chemoattractant prot
A/Reference number: A53477; MUID:94195821; PMID:8146186
A/Accession: 138463
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-360 <RES>
A/Cross-references: EMBL:U03905; NID:G472557; PIDN:AAA19120.1; PID:G472558
C/Genetics:
A/Genes: GDB:CMKBR2
A/Cross-references: GDB:337364; OMIM:601267
A/Map position: 3p21-3p21
C/Superfamily: vertebrate rhodopsin
C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
F:3-10/Domain: transmembrane #status predicted <TM2>
F:81-100/Domain: transmembrane #status predicted <TM3>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:154-178/Domain: transmembrane #status predicted <TM4>
F:207-226/Domain: transmembrane #status predicted <TM5>
F:244-268/Domain: transmembrane #status predicted <TM6>
F:287-309/Domain: transmembrane #status predicted <TM7>
F:14/Binding site: carboxylate (Asn) (covalent) #status predicted
F:113-190/Disulfide bonds: #status predicted

Query Match 29.5%; Score 567.5; DB 2; Length 360;
Best Local Similarity 39.2%; Pred. No. 7.6e-40;
Matches 125; Conservative 64; Mismatches 113; Indels 17; Gaps 8;

QY 26 DEVTDDYIGDNTTVDYTLTPESSLSCKDVNFRAMFLPIMYSIICFVGLGNGLVLTYY 85

Db 18 EVVT-----TFPYD-YGAPCHKFDVQIGAQLLPPLYSVPIFGFGNMLVVLILIN 69

QY 86 FRKLKMTDTYLLNLAADVILFLTLTPFAVYSAKSWFGVHFCKLIPAIYKMSFSGML 145
70 CKKLKCLTDIYLLNLAISDLFLTLPLMAHSAANEMVFGNAMCKLFTGLYHIGVGGIF 129

QY 146 LILCISIDRYVAIYQAVSAHRRARVLLISKLSGSAIILATVLSIPELLYSDLRSSSE 205
130 FILLITIDRYLAIYVAHVA--LKARTVFGVTSVITWLVAVPASVPGIIFPKCKQEDSV 187

QY 206 QAMRCS-LITEHVEAFITIQVQWVIGFVPLPLMSFCYLVIRTLQARN-FERNKAIR 263
188 YV--CGPYPRGMNPHITM--RNILGLVLPPLIIVICSGILKTLRCRNEKSHRAVR 243

QY 264 VTIAVVVFIVFQLPYNGVLAQTVANFNITSTCELSKOLNIADYVTSIACVRCVNP 323
244 VIPTIMIVFLEFMPYNYIILNTFOEF-FGLSNCESTSQLDAQVETLGMTHCCINP 302

QY 324 FLVAFIVGKERNDIFKLFK 342
303 IIVAFVGEKFRYSVFFR 321

Db

RESULT 14
JQ1231
interleukin-8 receptor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: JQ1231; A46483
R/Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBoe, T.; Price, V.; Lyman, S.; Gerard
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A/Title: Molecular characterization of the interleukin-8 receptor.
A/Reference number: JQ1231; MUID:91378994; PMID:1898400
A/Accession: JQ1231
A/Molecule type: DNA
A/Residues: 1-355 <BEC>
A/Cross-references: UNIPROT:P21109; GB:M74240; NID:G165438; PIDN:AAA1375.1; PID:G165439
R/lee, J.; Huang, W.J.; Rice, G.C.; Wood, W.T.
J. Immunol. 148, 1261-1264, 1992
A/Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A/Reference number: A46483; MUID:92148149; PMID:1737938
A/Accession: A46483
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-355 <LEB>
A/Cross-references: GB:M28273; NID:G165440; PIDN:AAA31376.1; PID:G165441
A/Experimental source: neutrophils
A/Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.4%; Score 565; DB 2; Length 355;
Best Local Similarity 37.1%; Pred. No. 1.2e-39; Matches 114; Conservative 66; Mismatches 91; Indels 36; Gaps 4;

QY 63 IMYSIICFVGLGNGLVLTYYIFRKLKMTDTYLLNLAADVILFLTLTPFAVYSAKSW 122
49 VTIAVVPLSLGNSLVWLIVILYRSNSVTDVYLLNLAADLPLALMPFAVSKSGW 108

QY 123 VFGVHFCKLIPAIYKMSFSGMLLILCISIDRYVAIYQAV--VSAHRRARVLLISKLS 179
109 IFGFLPKCVSVSYKENVFSGILLACISVDRYLAIVATRTLLQKRH-----LVKPIG 162

QY 180 VGSAILATVLSIPEL-----YSDLRSSSEQAMRCSLITEHVEAFITIOV 225
163 LGIWLALSLSLPFLPQVPSPNNSVPCYBDLGHNTAKRM-----VLRT 209

QY 226 AQWVIGFVPLPLMSFCYLVIRTLQARNFERNKAIRVITAVVVFIVFQLPYNGVLA 285
210 LPHTGFLPPLVLMFCGFLTRTLFOAHMGQKRAHNVIRAVVILFLCMLPYNVLVA 269

QY 286 QTVANFNITSTCELSKOLNIADYVTSIACVRCVNPFLVAFIVGKERNDIFKLFK 345


```
Db      270 DILMRTVIGTQRNDIDRALDAEILGFLHSCLNPIIYAFIIGQNFNGFLMLAARG 329
Qy      346 CLSQEQL 352
Db      330 LRSKEFL 336
```

RESULT 15

S42628

G protein-coupled receptor GPCR6 - mouse

N:Alternate names: interleukin-8 receptor homolog; mubL1 protein

C:Species: Mus musculus (house mouse)

C:date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C:Accession: S42628; C48909

R:Kaiser, E.; Foerster, R.; Wolf, I.; Ebensperger, C.; Kuehl, W.M.; Lipp, M.

Eur. J. Immunol. 23, 2532-2539, 1993

A:title: The G protein-coupled receptor BLR1 is involved in murine B cell differentiation

A:Reference number: S42628; MUID:94009211; PMID:8405054

A:Accession: S42628

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-374 <RA1>

A:Cross-references: UNIPROT:Q04683; EMBL:X71788; NID:92598563; PIDN:CAA50673.1; PID:9433

R:Wilke, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G

Genomics 18, 175-184, 1993

A:title: Identification, chromosomal location, and genome organization of mammalian G-pro

A:Reference number: A48909; MUID:94116980; PMID:8288218

A:Accession: C48909

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 151-269 <WIL>

A:Cross-references: GB:120332; NID:9438798; PIDN:AAA16852.1; PID:9438799

A:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.3%; Score 562.5; DB 2; Length 374;
Best Local Similarity 35.2%; Pred. No. 2.1e-39;
Matches 121; Conservative 78; Mismatches 124; Indels 21; Gaps 8;

```
Qy      46 SLCSKRD---VRNFKAMFLPIWYSIIICFVGLLNGGLVLTLYIFKRLKMTDLYLNLAV 102
Db      38 NPGSTVEGPLLTSFKAVFMPVAISLIFLLGWMGNILVLTLERRHRRSSTETFLPHLAV 97
Qy      103 ADILFLLTLPEFMAVSAKSVFVGFHFKLIFAIYKMSFSGMLLLCISIDRYVAIVQAV 162
Db      98 ADLLVFLIPFNAVBSGVGVLTGFLCKVYIALHKINFCSSILVACIADRYLAIVHAV 157
Qy      163 SAHRHRARVLLSKLSCVGSAILATVLSIPELLYSDL-QRSSSEQAMRCSLITEH---VE 218
Db      158 --HAYRRRLLSIHITCTALMAGFLFALPELLFAKVGQPHNNDLPLQCTFSQENEAEER 215
Qy      219 APTTIOVAGMVGFLVPLPLAMSCYLIYIRTLQA-RNPERKAIKYIIVVVVPIVFOQL 277
Db      216 AMFTSRFLYHIGFLPMLVMGWCYGVVRRLLQAQRPRQAKAVRAVAILVTSIFPLCWS 275
Qy      278 PYNGVVLTAQTVAFNITSTCELSKQNLINAYDVTYSLACVRCVNPFLYAFIGVKFRNDI 337
Db      276 PYHIVIFLDTLERLKAVNSCELSGYLSVAITLCEFLGLAHCLINPMLYTFAGVKFRSDL 335
Qy      338 FYLFKDLGCLISQEQLRQ---WSSCRHRRSSMSVEAETTTFS 377
Db      336 SRLTLKLGCGAPASLQCLFPNW-----RKSSLS-ESNATSLT 372
```

Search completed: February 25, 2005, 02:23:43
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 25, 2005, 02:06:32 ; Search time 176 Seconds
(without alignments)
1099.806 Million cell updates/sec

Title: US-10-749-990-2

Perfect score: 1922
Sequence: 1 MDLGRKMSVLLVALLVIFQ.....RHRRSSMSVEAEITTFSP 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_sprot;
2: uniprot_trembl;

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1907	99.2	378	1	CRK7_HUMAN
2	1889	98.3	378	2	Q8H2R6
3	1776	92.4	380	2	O861S1
4	1701	88.5	378	2	O8C8A2
5	1696	88.2	378	1	CRK7_MOUSE
6	1695	88.2	378	2	Q6U2D6
7	1131	58.8	246	2	Q6JXL2
8	1097.5	57.1	358	2	O6GP68
9	758.5	39.5	357	1	CRK9_HUMAN
10	758.5	39.5	359	2	Q9UQ06
11	748	38.9	359	1	CRK3_MOUSE
12	743.5	38.7	359	2	O8CH33
13	740.5	38.5	357	2	O6YT46
14	740.5	38.5	359	2	O6YT47
15	707.5	36.8	374	1	CRK6_HUMAN
16	703	36.6	357	1	CRK6_MOUSE
17	702	36.5	374	2	Q8H2E7
18	692	36.0	357	2	Q9R1V0
19	681	35.4	358	2	O42444
20	662	34.4	359	2	Q76LB9
21	655.5	34.1	351	2	Q9E0L6
22	654.5	34.1	341	2	O6YTM4
23	650.5	33.8	351	2	Q9ERH5
24	648.5	33.7	356	2	Q63ZL5
25	643	33.5	350	1	CRKB_HUMAN
26	629.5	32.8	350	2	Q924I3
27	627.5	32.6	350	2	O8C0M1
28	626.5	32.6	350	2	O8O2M9
29	618	32.2	350	1	CRKB_BOVIN
30	614	31.9	360	1	CRK4_HUMAN
31	609	31.7	360	2	Q8MJT8

32	603	31.4	360	2	Q91ZH4	Q91ZH4
33	601.5	31.3	382	2	Q70ZB3	Q70ZB3
34	599.5	31.2	361	2	Q8VHP3	Q8VHP3
35	598.5	31.1	342	1	CRK6_CERAE	Q189D3
36	598.5	31.1	343	1	CRK6_MACM	Q9X45
37	597	31.1	342	1	CRK6_MACNE	Q19024
38	595.5	31.0	343	1	CRK6_MACFA	Q9B46
39	595	31.0	342	1	CRK6_PANTR	Q9TV16
40	595	31.0	360	1	CRK4_MOUSE	P51680
41	591.5	30.8	343	2	Q9N0Z0	Q9N0Z0
42	588.5	30.6	342	1	CRK6_HUMAN	Q00574
43	588.5	30.6	342	2	Q9HCAS	Q9HCAS
44	588	30.6	359	2	Q9TUS4	Q9TUS4
45	585	30.4	339	2	Q9TUS3	Q9TUS3

ALIGNMENTS

RESULT 1	CRK7_HUMAN	STANDARD;	PRT;	378 AA.
AC	P32248			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	C-C chemokine receptor type 7 precursor (C-C CRK-7) (CC-CRK-7) (CCR-7)			
DE	(MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)			
DE	(EBI1) (BLR2).			
GN	Name=CRK7; Synonym=CKBR7, EBI1, EVI1;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93188173; PubMed=8383238;			
RA	Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,			
RA	Kieff E.;			
RT	"Protein-Barr virus-induced genes: first lymphocyte-specific G			
RT	protein-coupled peptide receptors.";			
RL	J. Virol. 67:2209-2220(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=95154835; PubMed=7651893;			
RA	Schweickart V.L., Raport C.U., Godiska R., Byers M.G., Eddy R.L. Jr.,			
RA	Shows T.B., Gray P.W.;			
RT	"Cloning of human and mouse EBI1, a lymphoid-specific G-protein-			
RT	coupled receptor encoded on human chromosome 17q12-q21.2.";			
RL	Genomics 23:643-650(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Mak S.T., Wang J., Hsieh F.,			
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Bromstein M.J., Ueda T.B., Tohivukl S., Carninci P., Prange C.,			
RA	Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richard S., Morley K.C., Hale S., Garcia A.N., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smilus D.E.,			
RA	Schmarch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			

RT and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator
CC of EBV effects on B lymphocytes or of normal lymphocyte functions.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in various lymphoid tissues and
CC activated B and T lymphocytes, strongly up-regulated in B cells
CC infected with Epstein-Barr virus and T cells infected with
CC herpesvirus 6 or 7.
CC -1- INDUCTION: By EBV.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC
DR EMBL, L08176; AAA58615.1; -
DR EMBL, L31584; AAA74230.1; -
DR EMBL, L31582; AAA74230.1; JOINED.
DR EMBL, L31583; AAA74230.1; JOINED.
DR EMBL, L31581; AAA74231.1; -
DR EMBL, BC035343; AAH35343.1; -
DR PIR, A45680; A45680.
DR PIR, B55735; B55735.
DR HSSP, P34996; 1DD0.
DR Genew; HGNC:1608; CCR7.
DR MIM: 600242; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004950; F:chemokine receptor activity; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. .); TAS.
DR GO; GO:0006935; P:chemotaxis; TAS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR001718; CC_7_receptor.
DR InterPro; IPR000355; Chemokine_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 25 378
FT DOMAIN 25 59
FT TRANSMEM 60 86
FT DOMAIN 87 95
FT TRANSMEM 117 130
FT DOMAIN 131 152
FT TRANSMEM 153 170
FT TRANSMEM 171 191
FT DOMAIN 192 219
FT TRANSMEM 220 247
FT DOMAIN 248 263
FT TRANSMEM 264 289
FT TRANSMEM 290 313
FT TRANSMEM 314 331
FT DOMAIN 332 378
FT CARBOHYD 36 36
FT DISULFID 129 210
FT CONFLICT 182 183
FT CONFLICT 337 337
SQ SEQUENCE 378 AA; 42874 MW; D4CB4213841A1BD4 CRC64;
Query Match 99.2%; Score 1907; DB 1; Length 378;
Best Local Similarity 99.2%; Pred. No. 7e-106;
Matches 375; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDLGKPMKSVLVALLVYI PQCGLCODEVTDVYIGDNTVDYTLFESLCSKKDVRNFKAMF 60
DB 1 MDLGKPMKSVLVALLVYI PQCGLCODEVTDVYIGDNTVDYTLFESLCSKKDVRNFKAMF 60
QY 61 LPIKMSIICFVGLGNGVLVLYIYIFPKRLKTWDTDTYTLNLAVADILFLTLTFFMAYSAK 120
DB 61 LPIKMSIICFVGLGNGVLVLYIYIFPKRLKTWDTDTYTLNLAVADILFLTLTFFMAYSAK 120
QY 121 SWVGFVHFKLIPAIYKMSFFSGMLLLICISIDRYVAIVQAVSANRHRARVLLISKLCV 180
DB 121 SWVGFVHFKLIPAIYKMSFFSGMLLLICISIDRYVAIVQAVSANRHRARVLLISKLCV 180
QY 181 GSALLATLSTPELILYSDLSORSSSQAMRCSLITHEVEAFITIOYAVONIGFVLPLAMS 240
DB 181 GSWLLATVLSPELILYSDLSORSSSQAMRCSLITHEVEAFITIOYAVONIGFVLPLAMS 240
QY 241 PCYVLIITLLOARFENRKAIKVIAVWVFIVFQLPNGVLAQTVA NFNTSSTCEL 300
DB 241 PCYVLIITLLOARFENRKAIKVIAVWVFIVFQLPNGVLAQTVA NFNTSSTCEL 300
QY 301 SKQNLIAVDVYSLACVRCVNPFLYAFI GVEFNDIFKLFQDLGCLSGEQLRQSSCRH 360
DB 301 SKQNLIAVDVYSLACVRCVNPFLYAFI GVEFNDIFKLFQDLGCLSGEQLRQSSCRH 360
QY 361 IRRSSMSVEAEFTTTFSP 378
DB 361 IRRSSMSVEAEFTTTFSP 378
RESULT 2
Q8H2R6 PRELIMINARY; PRT; 378 AA.
ID Q8H2R6
AC Q8H2R6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CC chemokine receptor 7.
GN Name=CCR7;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22471764; PubMed=12406887; DOI=10.1182/blood-2002-08-2653;
RA Choi Y.K., Fallett B.A., Murphy-Corb M.A., Reinhardt T.A.;
RT "Simian immunodeficiency virus dramatically alters expression of
RT homeostatic chemokines and dendritic cell markers during infection in
RT vivo.";
RT Blood 101:1684-1691(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL, AF508731; AAN47099.2; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR001718; CC_7_receptor.
DR InterPro; IPR000355; Chemokine_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00641; CCHEMOKINER.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 378 AA; 42876 MW; D031BB48B29F08EF CRC64;
Query Match 98.3%; Score 1889; DB 2; Length 378;
Best Local Similarity 98.7%; Pred. No. 8.2e-105;

Matches 373; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLGKPMKSVLVVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRNFKAMF 60
 DB 1 MDLGKPMKSVLVVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRNFKAMF 60
 QY 61 LPIWMSIICFVGLGNGLVLLVYIYFKRLKMTDTYLLNLAVADILFLTLTPMAYSAK 120
 DB 61 LPIWMSIICFVGLGNGLVLLVYIYFKRLKMTDTYLLNLAVADILFLTLTPMAYSAK 120
 QY 121 SWVFGVHFCCKLIFAIYKMSFSGMMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 180
 DB 121 SWVFGVHFCCKLIFAIYKMSFSGMMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 180
 QY 181 GSAILATVLSIPELYSIDLORSSSEQAMRCSLITTEHVEAFITIQVAMVIGFLVPLIAMS 240
 DB 181 GSAILATVLSIPELYSIDLORSSSEQAMRCSLITTEHVEAFITIQVAMVIGFLVPLIAMS 240
 QY 241 FCYLVIIIRTLQARNFERNKAIKVIAVVVPIVFPQLPYNGVLAQTVAANFNITSTCEL 300
 DB 241 FCYLVIIIRTLQARNFERNKAIKVIAVVVPIVFPQLPYNGVLAQTVAANFNITSTCEL 300
 QY 301 SKQMLNAYDVYTSIACVRCVNPFLYAFIGVKEFNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 DB 301 SKQMLNAYDVYTSIACVRCVNPFLYAFIGVKEFNDIFKLFKDLGCLSQEQLRQWSSCRH 360
 QY 361 IRRSSMSVEAETTTTSP 378
 DB 361 IRRSSMSVEAETTTTSP 378

RESULT 3

0861S1 PRELIMINARY; PRT; 380 AA.

AC 0861S1; 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Chemokine receptor 7 (Chemokine (C-C motif) receptor 7).
 GN Name=CCR7;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCB1_TaxID=9823;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Muneta Y., Awata T., Uenishi H.,
 RN Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA Shinkai H., Muneta Y., Awata T., Uenishi H.,
 RT "Abstract Molecular cloning and chromosomal assignment to
 RT SSC12P13-SP1 of swine chemokine receptor CCR7.";
 RT Cytogenet. Genome Res. 101:155-160(2003).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Uenishi H., Eguchi T., Suzuki K., Sawazaki T., Toki D., Shinkai H.,
 RA Okumura N., Hamaishi N., Awata T.,
 RT "PDB (Pig EST Data Explorer): construction of a database for ESTs
 RT derived from porcine full-length cDNA libraries.";
 RT Nucleic Acids Res. 32:D484-D488(2004).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AB090356; BAC57561.1; -;
 DR EMBL; AB090872; BAC57929.1; -;
 DR EMBL; AB090870; BAC57929.1; JOINED.
 DR EMBL; AB090871; BAC57929.1; JOINED.
 DR EMBL; AB116555; BAD06309.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR001718; CC_7_receptor.
 DR InterPro; IPR000355; Chm_kine_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR00641; CHEMOKINER7.
 DR PRINTS; PR00237; GPCR_RHODOPN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1.
 DR PROSITE; PS02622; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 380 AA; 42851 MW; 948B2794C6A76AD8 CRC64;

Query Match 92.4%; Score 1776; DB 2; Length 380;

Best Local Similarity 91.3%; Pred. No. 4.3e-98;
 Matches 347; Conservative 16; Mismatches 15; Indels 2; Gaps 2;

QY 1 MDLGKPM-KSVLVVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRNFKAM 59
 DB 1 MDLGKPMKSVLVVALLVIFQVCLCODEVTDDYIGNTTVDYTLFESLCSKQDVRNFKAM 60
 QY 60 LPIWMSIICFVGLGNGLVLLVYIYFKRLKMTDTYLLNLAVADILFLTLTPMAYSAK 119
 DB 60 LPIWMSIICFVGLGNGLVLLVYIYFKRLKMTDTYLLNLAVADILFLTLTPMAYSAK 120
 QY 120 KSWVFGVHFCCKLIFAIYKMSFSGMMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 179
 DB 120 KSWVFGVHFCCKLIFAIYKMSFSGMMLLLCISIDRYVAIVQAVSAHRHRAVLLISKLS 180
 QY 180 VGSAILATVLSIPELYSIDLORSSSEQAMRCSLITTEHVEAFITIQVAMVIGFLVPLIAMS 239
 DB 180 VGSAILATVLSIPELYSIDLORSSSEQAMRCSLITTEHVEAFITIQVAMVIGFLVPLIAMS 240
 QY 240 SPICYLVIIIRTLQARNFERNKAIKVIAVVVPIVFPQLPYNGVLAQTVAANFNITST-C 298
 DB 241 SPICYLVIIIRTLQARNFERNKAIKVIAVVVPIVFPQLPYNGVLAQTVAANFNITST-C 300
 QY 299 ELISKQMLNAYDVYTSIACVRCVNPFLYAFIGVKEFNDIFKLFKDLGCLSQEQLRQWSSC 358
 DB 301 ELISKQMLNAYDVYTSIACVRCVNPFLYAFIGVKEFNDIFKLFKDLGCLSQEQLRQWSSC 360
 QY 359 RHRRSSMSVEAETTTTSP 378
 DB 361 RHRRSSMSVEAETTTTSP 380

RESULT 4

08CAS2 PRELIMINARY; PRT; 378 AA.

AC 08CAS2; 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched
 DE library, clone:A130067M15 product:chemokine (C-C) receptor 7, full
 DE insert sequence.
 GN Name=Ccr7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCB1_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RT Meth. Enzymol. 303:19-44(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";

RN Nature 409:685-690(2001).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA the FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RL Nature 420:563-573(2002).
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
 RT "Normalization and substructure of cap-trapper-selected cDNAs to
 RL prepare full-length cDNA libraries for rapid discovery of new genes";
 RX Genome Res. 10:1617-1630(2000).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20530913; Pubmed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Saeki N., Carninci P.,
 RA Kono H., Akiyama T., Nishi K., Kikunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishi Y., Nakamura S., Hazama N., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer.";
 RX Genome Res. 10:1757-1771(2000).
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanda K.,
 RA Karch H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Saeki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takahashi A., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Yamatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBS databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC EMBL: AK037965; BAC29909.1; -.
 DR MGD: MGI:103011; Ccr7.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0016493; F:C-C chemokine receptor activity; IMP.
 DR GO: GO:0006935; P:chemotaxis; IMP.
 DR GO: GO:0006955; P:immune response; IMP.
 DR InterPro: IPR001718; CC 7 receptor.
 DR InterPro: IPR000355; Chem_kinase_receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: Pf00001; 7tm_1; 1.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PRINTS: PR00641; CHEMOKINERF.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G_PROTEIN_RECP_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 QO SEQUENCE 378 AA; 42855 MW; F02745198B59683 CXC64;

```

Db      1 MDPEKPRKRVLVVALLVITFOVCEQODEVDITDYGENTTDYITLESYCFPKDVRNFAWF 60
QY      61 LPIMYSIICFVGLGNGVLLVITYFRRLKTMDTYLLNLAVADILELLTLPFWA5AAK 120
Db      61 LPLAVSYICFVGLGNGVLLITYFRRLKTMEDTYLLNLAVADILELLTLPFWA5EAK 120
QY      121 SWVGCHAFCKLIFAIYKMSPFSSGMLLLCISIDRYVAIVQVNSHRRRAVLLSKLSCV 180
Db      121 SMIVGVVLCGKIFGIYKLSFFSGMLLLCISIDRYVAIVQVNSHRRRAVLLSKLSCV 180
QY      181 GSALLATVLSIPELLYSDLORSSESOAMRCSLIENHEAFITIOVAOMVIGFLVPLAMS 240
Db      181 GIMWALFLSIPELLYSGLOKNSSEDTKRSLSVAQVBALEITIOVQOMVIGFLVPLAMS 240
QY      241 FCYLIIVIRTLQANFERNRKAIKYIIAVVVVFIVFQOLPYNGVLAQTVAANFNITSCEL 300
Db      241 FCYLIIVIRTLQANFERNRKAIKYIIAVVVVFIVFQOLPYNGVLAQTVAANFNITSSET 300
QY      301 SKQINIAVDYVYSIACRCACCNPLVAFVIGKPRNDIFKLPKDLGCLSGOQLROMSSCRH 360
Db      301 SKQINIAVDYVYSIASVCCNPNPLVAFVIGKPRSDLFKLPKDLGCLSGOQLROMSSCRH 360
QY      361 IRSSMSVEAEATTTTSP 378
Db      361 VRNASVSMEAETTTTSP 378

RESULT 5
CKR7_MOUSE
ID CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7)
DE (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)
DE (EBI1).
GN Name=Ccr7; Synonyms=Cmbb17, Eb11, Eb11h;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=95154835; Pubmed=7851893;
RA Schweickart V.L., Raport C.J., Godliska R., Byers M.G., Eddy R.L. Jr.,
RA Shows T.B., Gray P.W.;
RT "Cloning of human and mouse EBI1, a lymphoid-specific G-protein-
RT coupled receptor encoded on human chromosome 17q12-q21.2.";
RL Genomics 23:643-650(1994).
CC -1- FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator
CC of EBV effects on B lymphocytes or of normal lymphocyte functions.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U31580; AAA74232.1; -.
DR PIR; A55735; A55735.
DR MGD; MGI:103011; Ccr7.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IMP.
DR GO; GO:0006935; P:chemotaxis; IMP.
DR GO; GO:0006955; P:immune response; IMP.
DR InterPro; IPR001718; CC_7_receptor.
DR InterPro; IPR000355; Cmkine_receptor.

```

```
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 24
FT CHAIN 1 378
FT DOMAIN 25 59 C-C chemokine receptor type 7.
FT TRANSMEM 60 86 Extracellular (Potential).
FT DOMAIN 87 95 1 (Potential).
FT TRANSMEM 96 116 Cytoplasmic (Potential).
FT DOMAIN 117 130 2 (Potential).
FT TRANSMEM 131 152 Extracellular (Potential).
FT DOMAIN 153 170 3 (Potential).
FT TRANSMEM 171 191 Cytoplasmic (Potential).
FT DOMAIN 192 219 4 (Potential).
FT TRANSMEM 220 247 Extracellular (Potential).
FT DOMAIN 248 263 5 (Potential).
FT TRANSMEM 264 289 Cytoplasmic (Potential).
FT DOMAIN 290 313 6 (Potential).
FT TRANSMEM 314 331 Extracellular (Potential).
FT TRANSMEM 332 378 7 (Potential).
FT CARBOHYD 36 36 Cytoplasmic (Potential).
FT DISULFID 129 210 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 378 AA; 42941 MW; 42941 MW; ACBIA422CF54A54 CRC64;

Query Match
Best Local Similarity 86.0%; Score 1696; DB 1; Length 378;
Matches 325; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDTYLLFBSLSCKKQVRNFKAMF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDTYLLFBSLSCKKQVRNFKAMF 60
QY 61 LPIKMSIIFGVGLNGVLLVITYYFKRLKMTDPTYLNLAAVDILFLTLPPMAVSAK 120
DB 61 LPIKMSIIFGVGLNGVLLVITYYFKRLKMTDPTYLNLAAVDILFLTLPPMAVSAK 120
QY 121 SWFGVHFCKLFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
QY 122 SWIFGVLCKGIFGIYKLSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 122 SWIFGVLCKGIFGIYKLSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
QY 181 GSAILATVLSIDELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLPAMS 240
DB 181 GSAILATVLSIDELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLPAMS 240
QY 181 GIMMLALFISIDELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLPAMS 240
DB 181 GIMMLALFISIDELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLPAMS 240
QY 241 FCYLVIRTLQARNFERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSCEL 300
DB 241 FCYLVIRTLQARNFERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSCEL 300
QY 241 FCYLVIRTLQARNFERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSCEL 300
DB 241 FCYLVIRTLQARNFERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSCEL 300
QY 301 SKQNLAVDVTSLSACVRCVNPFLVAFIGVFRNDIFPLFDLGLGCLSGEQLRQWSSCRH 360
DB 301 SKQNLAVDVTSLSACVRCVNPFLVAFIGVFRNDIFPLFDLGLGCLSGEQLRQWSSCRH 360
QY 301 SKQNLAVDVTSLSACVRCVNPFLVAFIGVFRNDIFPLFDLGLGCLSGEQLRQWSSCRH 360
DB 301 SKQNLAVDVTSLSACVRCVNPFLVAFIGVFRNDIFPLFDLGLGCLSGEQLRQWSSCRH 360
QY 361 IRRSSMSVEATTTTTFSP 378
DB 361 IRRSSMSVEATTTTTFSP 378
QY 361 VRNASVSMVEATTTTTFSP 378
DB 361 VRNASVSMVEATTTTTFSP 378

RESULT 6
Q6JXL2 PRELIMINARY; PRT; 378 AA.
AC Q6JXL2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Chemokine receptor 7-like protein.
GN Name=CCR7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BN; TISSUE=Lymph node;
RA Quintini G., Voland B., Hoffmeyer A.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AY379972; AAR24573.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR001718; Cc 7 receptor.
DR InterPro: IPR000355; Chemkine receptor.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00657; CCHMOKINER.
DR PRINTS: PR00641; CHEMOKINER7.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 378 AA; 42821 MW; A015E711DC4B521F CRC64;

Query Match
Best Local Similarity 85.4%; Score 1695; DB 2; Length 378;
Matches 323; Conservative 29; Mismatches 26; Indels 0; Gaps 0;

QY 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDTYLLFBSLSCKKQVRNFKAMF 60
DB 1 MDLGRKMSVLLVALLVIFQVCLCODEVTDDYIGDNTTYDTYLLFBSLSCKKQVRNFKAMF 60
QY 61 LPIKMSIIFGVGLNGVLLVITYYFKRLKMTDPTYLNLAAVDILFLTLPPMAVSAK 120
DB 61 LPIKMSIIFGVGLNGVLLVITYYFKRLKMTDPTYLNLAAVDILFLTLPPMAVSAK 120
QY 121 SWFGVHFCKLFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 121 SWFGVHFCKLFAIYKMSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
QY 122 SWIFGVLCKGIFGIYKLSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
DB 122 SWIFGVLCKGIFGIYKLSFFSGMLLLCISIDRYVAIVQAVSAHRHRAVLLISLSCV 180
QY 181 GSAILATVLSIDELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLPAMS 240
DB 181 GSAILATVLSIDELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLPAMS 240
QY 181 GIMTLAFLSIDELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLPAMS 240
DB 181 GIMTLAFLSIDELYSIDLRSSSEQAMRCSLITHEVEAFITIQVQMYIGFVPLPAMS 240
QY 241 FCYLVIRTLQARNFERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSCEL 300
DB 241 FCYLVIRTLQARNFERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSCEL 300
QY 241 FCYLVIRTLQARNFERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSCEL 300
DB 241 FCYLVIRTLQARNFERKAIKVIIVVVFIVFQLPYNGVLAQTVANFNITSSCEL 300
QY 301 SKQNLAVDVTSLSACVRCVNPFLVAFIGVFRNDIFPLFDLGLGCLSGEQLRQWSSCRH 360
DB 301 SKQNLAVDVTSLSACVRCVNPFLVAFIGVFRNDIFPLFDLGLGCLSGEQLRQWSSCRH 360
QY 301 SKQNLAVDVTSLSACVRCVNPFLVAFIGVFRNDIFPLFDLGLGCLSGEQLRQWSSCRH 360
DB 301 SKQNLAVDVTSLSACVRCVNPFLVAFIGVFRNDIFPLFDLGLGCLSGEQLRQWSSCRH 360
QY 361 IRRSSMSVEATTTTTFSP 378
DB 361 IRRSSMSVEATTTTTFSP 378
QY 361 VRTSVSMVEATTTTTFSP 378
DB 361 VRTSVSMVEATTTTTFSP 378

RESULT 7
Q6JXL2 PRELIMINARY; PRT; 246 AA.
AC Q6JXL2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Chemokine receptor 7 (Fragment).
GN Name=CCR7;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxId=9913;
[1]
```

```

RP SEQUENCE FROM N.A.
RA Werling D.;
RA Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY277742; AAQ18436.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . ; IEA.
DR InterPro; IPR001718; CC 7 receptor.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00641; CHEMOKINER7.
DR PRINTS; PR00237; GPCRKHODOPEN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_REC_P1_2; 1.
DR KW Receptor.
FT NON TER
SQ SEQUENCE 246 AA; 27621 MW; 357BCD127F463608 CRC64;

Query Match 58.8%; Score 1311; DB 2; Length 246;
Best Local Similarity 90.7%; Pred. No. 6,6e-60;
Matches 224; Conservative 13; Mismatches 8; Indels 2; Gaps 2;

QY 133 FAIYKMSFSSGKLLLCISIDRYVAIVQAVSAHRRARLTLISKSCVSALATVLSIP 192
DB 1 FAIYKMSFSSGK-LLLCISIDRYVAIVQAVSAHRRARLTLISKSCIGIMWLAIVLSIP 59
QY 193 ELLYSDLRSSSEQAMRCSLTIEHVEAFITIQAVQVIGFLPPLAMSPCYVIIRTLIQ 252
DB 60 EWMYSGIQKSSSEQLRCSLTIEHVEAFITIQAVQVIGFLPPLAMSPCYVIIRTLIQ 119
QY 253 AANFERNAIKYIIAVVVFVIFQLPYNGVLAQTVANFNITST-CELSKQNTAYDVT 311
DB 120 AANFERNAIKYIIAVVVFVIFQLPYNGVLAQTVANFNITSTGSCSLKQNTAYDVT 179
QY 312 YSLACVRCVNPFLAIFGVKFRANDIFKLFKDLGCLSGEQALQMSSCRIRSSMSVEAE 371
DB 180 YSLACVRCVNPFLAIFGVKFRNDLFLKLFKDLGCLSGEQALQMSSCRIRSSMSVEAE 239
QY 372 TTTTFSP 378
DB 240 TTTTTFSP 246

```

```

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman A., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences."
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002) .
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SpLeen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RA initiative."
RA Dev. Dyn. 225:384-391 (2002) .
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=SpLeen;
RA Klein S., Gerhard D.S.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; BC073273; AAH73273.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . ; IEA.
DR InterPro; IPR001718; CC 7 receptor.
DR InterPro; IPR000355; Chkline receptor.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR00641; CHEMOKINER7.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_REC_P1_2; 1.
DR G-protein coupled receptor; Transmembrane.
KW SEQUENCE 358 AA; 40555 MW; D1F37C148823CAD5 CRC64;

Query Match 57.1%; Score 1097.5; DB 2; Length 358;
Best Local Similarity 56.6%; Pred. No. 8,7e-58;
Matches 206; Conservative 70; Mismatches 81; Indels 7; Gaps 3;

QY 16 LVIFQVCLCODEVTDYDYGNTTYDTLPESLCSKQDVNPRKAMFLPMYSLICFVGLG 75
DB 1 MATFQLAVGEDVNSYDENVPPYSTMDYSDLQVQCQGDVTRFPRSSFLPMYTLICLVGLAG 60
QY 76 NGLVVLITYFKRLTMTDYLTLNLAIVADILFLTLPMFVSAASQWFGVFKLIPAI 135
DB 61 NGLVWIRLYFRKLNQTDYMLNLAIDLIVFLTLPMFVSAASQWFGVSMCKIITCL 120
QY 136 YKMSFSSGKLLLCISIDRYVAIVQAVSAHRRARLTLISKSCVSAIATVLSIP 195
DB 121 YKMSFSSGKFLMCMQSMERYPAIVQAPSAHRRARLTLISKSGIWMFAFLSIP 180
QY 196 YSDLRSSSEQAMRCSLTIEHVEAF-ITIQAVQVIGFLPPLAMSPCYVIIRTLQAR 254
DB 181 YSGVANNNGS--VNMCIIFSNSIOSLSAKLTKISQMFEGFLPLITALCYCMIRKTLQAR 238
QY 255 NPERKAIKVIIVAVVVFIVQLPVGVLVLAQTVANFNITSTGSLSKQNTAYDVTSL 314
DB 229 NPERKAIKVIIVAVVVFIVQAPLPTNSVWLITFPN---GTDCAASKLADADVITSL 294
QY 315 ACVRCVNPFLAIFGVKFRNDIFKLFKDLGCLSGEQALQMSSCRIRSSMSVEAETTT 374
DB 295 ACVRCVNPFLAIFGVKFRNDIFKLFKDLGCLSGEQALQMSSCRIRSSMSVEAETTT 354
QY 375 TFSP 378

```


Db 355 TESP 358

RESULT 9

CCR9_HUMAN STANDARD; PRT; 357 AA.

AC P51686; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE C-C chemokine receptor type 9 (C-C CKR-9) (CC-CCR-9) (CCR-9) (GPR-9-6).

GN Name=CCR9; Synonyms=CKCR9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RA Laurens L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M., Bonner T.L.;

RU Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RA Warren C.N., Atonstam R.S., Sharma S.V.;

RT "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";

RU Submitted (Feb-2003) to the EMBL/GenBank/DBJ databases.

RP CHARACTERIZATION.

RX Zaballos A., Gutierrez J., Varona R., Ardevin C., Marquez G.;

RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the receptor for the chemokine TECK.";

RL J. Immunol. 162:5671-5675(1999).

CC -1- FUNCTION: Receptor for chemokine SCY25/TECK. Subsequently transduces a signal by increasing the intracellular calcium ions level. Alternative coreceptor with CD4 for HIV-1 infection.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Highly expressed in the thymus and low in lymph nodes and spleen.

CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

CC EMBL: U45982, AAA93319.1, --

CC EMBL: AT242127, AA092294.1, --

CC GeneW: HGNC:1610; CCR9.

DR MIM: 604738; --

DR GO: GO:0005887; C: integral to plasma membrane; TAS.

DR GO: GO:0004950; F: chemokine receptor activity; TAS.

DR GO: GO:0006968; P: cellular defense response; TAS.

DR GO: GO:0006935; P: chemotaxis; TAS.

DR GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.

DR GO: GO:0007186; P: G-protein coupled receptor protein signaln. .; TAS.

DR InterPro: IPR004069; CC 9 receptor.

DR InterPro: IPR000355; Chkline_receptor.

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PRO1531; CHEMOKINER9.

DR PROSITE: PS00237; GPCR_HODOPSIN.

DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.

DR PROSITE: PS00237; G_PROTEIN_RECP_FL_2; 1.

KW G-protein coupled receptor; Glycoprotein; Transmembrane.

FT DOMAIN 1 37

FT TRANSMEM 38 64

FT 1 (Potential).

PT DOMAIN 65 73

PT TRANSMEM 74 94

FT DOMAIN 95 108

FT TRANSMEM 109 130

FT DOMAIN 131 148

FT TRANSMEM 149 169

FT DOMAIN 170 198

FT TRANSMEM 199 226

FT DOMAIN 227 242

FT TRANSMEM 243 268

FT DOMAIN 269 292

FT TRANSMEM 293 310

FT DOMAIN 311 357

FT CARBOHYD 20 20

FT DISULFID 107 186

SO SEQUENCE 357 AA; 40713 MW; 96982E0B922F6531 CRC64;

Query Match 39.5%; Score 758.5; DB 1; Length 357;

Best Local Similarity 42.0%; Pred. No. 1.2e-37;

Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;

QY 28 VTDDYIGDNT-----VDYTFESLCKSKDVRNPKAMPPIWYSICFVGLGGLVLT 82

DB 1 MADDYSESTSMEDYVNFNFTDPYCEKNNVROFASHFLPPLYVIVIGALGNSLVILV 60

QY 83 YIYFKELKMTDTYLLNLAVADILFLTLPPNAYSNAKSWPGVHPCKLIFAYKNSPFS 142

DB 61 YWYCRVKMTDMFLNLAIADLLFLVTLPPNAAADQMKPQTFMCKVNSWYKNNFYIS 120

QY 143 GMLLLICISIDRYVAIVQAVSAHRHARVLLISKSCVSALIAATVLSIPELLYSDLQRS 202

DB 121 CVLLIMCISVDRIYAIQAQMARHTWREKRLVSKVCFTIWTVAALCIPELIYSQIKER 180

QY 203 SSEQARGSLI-----TEHVEAFITIOVAQWIGFLVLLMSFCYLVITRTLGARNF 256

DB 181 SG--IAICTWVPDSSTYKSKSVLTLYK--ILGFLLPWNACCTTIITHTLQKKS 235

QY 257 ERNKAIKVIAVWVFIYFQLPNGVLAQTVAFNITSSTCELSKQNLNADVTYSLAC 316

DB 236 SKRKLKVTITVLTAVLVLSQFPYNCILVQTDIVAMFISNCAVSINIDICFQVGTIAF 295

QY 317 VRCCNPFLYALPGVFRNDIFKLFQDLGCLSGEQLRQNSGCH---IRRSMSVE 369

DB 296 FHSCLNPVLVYFVGFRFRDLVKTILKLGICISG---AQWVSFTRREGSKLSMLDE 349

RESULT 10

Q9U0Q6 PRELIMINARY; PRT; 369 AA.

AC Q9U0Q6; 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)

DE Chemokine receptor CCR9 (Chemokine (C-C motif) receptor 9, isoform A)

DE (CC chemokine receptor 9A).

GN Name=CCR9;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=99248139; PubMed=10229797;

RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the receptor for the chemokine TECK.";

RL J. Immunol. 162:5671-5675(1999).

RP SEQUENCE FROM N.A.

RP TISSUE=PCR rescued clones;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Alechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchek L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stagleon M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
RA Boask S.A., McKernan P.J., McKernan K.J., Malek J.A., Guarniere F.H.,
RA Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schen J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Yu C.-R., Feden K.W.C., Farber J.M.,
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AJ133337; CAB43477.1; -;
DR EMBL: BC069678; AAH69678.1; -;
DR EMBL: AF145439; AAH66699.1; -;
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR004069; CC_9_receptor.
DR InterPro: IPR000355; Chmkin_receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00657; CCHEMOKINER.
DR PRINTS: PR01531; CHEMOKINER.
DR PRINTS: PR00237; GPCRHDOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 369 AA; 42015 MW; F27CEA0CFB66844C CRC64;
SQ
Query Match 39.5%; Score 758.5; DB 2; Length 369;
Best Local Similarity 42.0%; Pred. No. 1.3e-37;
Matches 150; Conservative 78; Mismatches 106; Indels 23; Gaps 6;
QY 28 VDDYDIGNDT-----VDYLFESLCSKDVNFKAMFLPIWYITICFVGLNGIVLT 82
DB 13 MADDGSESTSMEDYVNFNFTDYCEKNVQFOPSHFLPILYVWLVGALGNSLVILV 72
QY 83 YLYFKRLKMTDTYLLNLAVADILFLTLFPVAVSAKSWGVHCKLIPAIYKMSFPS 142
DB 73 YVYCCRVKMTMDPLNLALADLFLVTLFPFAIAAADQMKQTFMCKVKNVSNMYCNKPS 132
QY 143 GMLLLCLISIDRYVAIVQAVSHRRARVLLISKLSCVSGAAILAVLVSIPELLYSDLORS 202
DB 133 CYLLIMCISVDRIYIAIAQAMRAHTWREKRLYSKVCFTIWTALALCIPILYISQIKER 192
QY 203 SSEQAMRGSLI-----TEHVAFTIOQAVNIGVFLVLLMSPCYVLIITTLQARNP 256
DB 193 SG--IATCMVPSDESTYLSKSAVLTKV--ILGFLEPVWVACCYTIIHTLLQAKKS 247
QY 257 EENKAKIVIAVWVFIQPLPYNQVVLAVQTVANFNITSTGELSKOLINAVDVTSLAC 316
DB 248 SKHAKLVITVLTLYFVLSQFPYNCILLVQITIDANAFISNCAVSNIDICQVOTIAP 307

QY 317 VRCNPPFLVYAFIGKFRNDIFKLPKDIGLSQDRLQWSSCRH-----IRSSMSVE 369
DB 308 FHSCLNPLVYFVGFRFRDVLTKLNKIGCISQ--AAQVSPTRREGSLKLSMILE 361
RESULT 11
CCR9_MOUSE STANDARD; PRT; 369 AA.
AC 09WDT7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 9 (C-C CCR-9) (CC-CCR-9) (CCR-9)
DE (Chemokine C-C receptor 10).
GN Name=Ccr9; Synonyms=cmbkr10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA MEDLINE=99248139; PubMed=10229797;
RT Zaballós A., Gutierrez J., Varona R., Ardavin C., Marquez G.,
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RT receptor for the chemokine TECK.";
J. Immunol. 162:5671-5675(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20069400; PubMed=10602049;
RX DOI=10.1002/1521-4141(200001)30:1<262::AID-IMMU262>3.0.CO;2-S;
RA Würl M.A., Philippe J.M., Nguyen C., Victorero G., Freeman T.,
RA Wooding P., Mazek A., Mattei M.-G., Møllisen M., Jordan B.R.,
RA Møllisen B., Carrier A., Naquet P.,
RT "The chemokine TECK is expressed by thymic and intestinal epithelial
RT cells and attracts TECK+ and single-positive thymocytes expressing
RT the TECK receptor CCR9.";
Eur. J. Immunol. 30:262-271(2000).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nishida I., Oshio N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schimpl L.M., Kapapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frezer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., Kling B.L.,
RA Kongaya A., Kurochkin I.V., Lee Y., Lenzhard B., Lyons P.A.,
RA Maglott D.R., Maltale L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Petrea G., Pezole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.B., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Warande Y., Wells C.,
RA Wilting L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaeunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
CC -1- FUNCTION: Receptor for chemokine SCYA25/TECK. Subsequently
transduces a signal by increasing the intracellular calcium ions

06YT46
ID 06YT46 PRELIMINARY; PRT; 357 AA.
AC 06YT46;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 9 isoform B.
GN Name=CCR9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AP006184; BAD08644.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR004069; CC_9_receptor.
DR InterPro; IPR000355; Cmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01531; CHEMOKINER9.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 357 AA; 40725 MW; 93F80F90F913337A CRC64;

Query Match 38.5%; Score 740.5; DB 2; Length 357;
Best Local Similarity 42.5%; Pred. No. 1.4e-36;
Matches 151; Conservative 70; Mismatches 111; Indels 23; Gaps 6;

QY 30 DDYIDNNTV-----DYTLFESLCSKDVNFKAWFLPIMYSIICFVGLAGLVLTYYI 84
DB 3 DDYGDATPSIEDYGNFTTDLFCCKKNHVRQFASHFLPLVWLVIVGAVGSLVILYYW 62
QY 85 YFKRLKMTDTYLLNLAVADILFLTLFPWYSAKSNVGVHFCKLIPAIYKMSFFSGM 144
DB 63 YCTRVKMTDMFLNLAIADLLFLVTLFPWMAIADQMKFOTFMCKVNVSMYKMFYSCV 122
QY 145 LLLLCISIDRYVAIYQAVSAHRRARVLLISLSCVGSAILATVLSIPELLYSDIQRSS 204
DB 123 LLMICISVDRIYALIAQAMRAQTWRQKRLLSKLVCFVWVMAALCIPELLYS--QVKEE 180
QY 205 EQAMCSLI-----TEHVEAFITIOAVQWYIGFVPLPLAMSFVYLVIIRTLQARNFER 258
DB 161 HDIACITWYVPSDESTNLKSAVLTAKV---ILGFPLPVVMAACCTIIIIHTLIQAKKSK 237
QY 239 NKAIIVIIAAVVVFLVFLQLPYNGVLAQTVANFNITSTCELSKQNTAIYDVYSLACVR 318
DB 228 HKALKVTITLVFLVFLSGFPYNCVLLVQTIIDAYTWFISSCAVSTNIDICFQVLTQIAFPH 297
QY 319 CCWNPFLYAFIGVKRRNDIFKLFDLGLCSQEQLRQMSCHN---IRSSMSV 369
DB 298 SCLNPLVLFVGERFRDLVKTLLKNGICISQ---AQWVSFTRREGSLKLSMLLB 349

RESULT 14
06YT47
ID 06YT47 PRELIMINARY; PRT; 369 AA.
AC 06YT47;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 9 isoform A (Chemokine C-C motif

DE receptor 9).
GN Name=CCR9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Eguchi T., Muneta Y., Awata T.,
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AP006184; BAD08644.1; -.
DR EMBL; AB119263; BAD12126.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR004069; CC_9_receptor.
DR InterPro; IPR000355; Cmkine_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01531; CHEMOKINER9.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_REC_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 369 AA; 41967 MW; DEBF76538600D620 CRC64;

Query Match 38.5%; Score 740.5; DB 2; Length 369;
Best Local Similarity 42.5%; Pred. No. 1.5e-36;
Matches 151; Conservative 70; Mismatches 111; Indels 23; Gaps 6;

QY 30 DDYIDNNTV-----DYTLFESLCSKDVNFKAWFLPIMYSIICFVGLAGLVLTYYI 84
DB 15 DDYGDATPSIEDYGNFTTDLFCCKKNHVRQFASHFLPLVWLVIVGAVGSLVILYYW 74
QY 85 YFKRLKMTDTYLLNLAVADILFLTLFPWYSAKSNVGVHFCKLIPAIYKMSFFSGM 144
DB 75 YCTRVKMTDMFLNLAIADLLFLVTLFPWMAIADQMKFOTFMCKVNVSMYKMFYSCV 134
QY 145 LLLLCISIDRYVAIYQAVSAHRRARVLLISLSCVGSAILATVLSIPELLYSDIQRSS 204
DB 135 LLMICISVDRIYALIAQAMRAQTWRQKRLLSKLVCFVWVMAALCIPELLYS--QVKEE 192
QY 205 EQAMCSLI-----TEHVEAFITIOAVQWYIGFVPLPLAMSFVYLVIIRTLQARNFER 258
DB 193 HDIACITWYVPSDESTNLKSAVLTAKV---ILGFPLPVVMAACCTIIIIHTLIQAKKSK 249
QY 259 NKAIIVIIAAVVVFLVFLQLPYNGVLAQTVANFNITSTCELSKQNTAIYDVYSLACVR 318
DB 250 HKALKVTITLVFLVFLSGFPYNCVLLVQTIIDAYTWFISSCAVSTNIDICFQVLTQIAFPH 309
QY 319 CCWNPFLYAFIGVKRRNDIFKLFDLGLCSQEQLRQMSCHN---IRSSMSV 369
DB 310 SCLNPLVLFVGERFRDLVKTLLKNGICISQ---AQWVSFTRREGSLKLSMLLB 361

RESULT 15
CCR6_HUMAN
ID CCR6_HUMAN STANDARD; PRT; 374 AA.
AC P51684; P78553; Q92846;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 6 (C-C CCR-6) (CC-CCR-6) (CCR-6) (LARC

DE receptor (GPR-C14) (GPCR4) (chemokine receptor-like 3) (CCR-L3)
 (DR66)
 GN Name=CCR6; Synonyms=CCR13, CCR6R6, GPR29, STRL22;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=97131465; PubMed=9169459; DOI=10.1074/jbc.272.23.14893;
 RA Baba M., Inai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,
 RA Nomiyama H., Yoshie O.,
 RT "Identification of CCR6, the specific receptor for a novel lymphocyte-
 RT directed CC chemokine LARC.";
 RL J. Biol. Chem. 272:14893-14898(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Laurens L., Modi W., Bonner T.I.,
 RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97040707; PubMed=8886020; DOI=10.1006/bbrc.1996.1595;
 RA Zaballo A., Varona R., Gutierrez J., Lind P., Marquez G.,
 RT "Molecular cloning and RNA expression of two new human chemokine
 RT receptor-like genes.";
 RL Biochem. Biophys. Res. Commun. 227:846-853(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA McCoy R., Perlmuter D.H.,
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224503; PubMed=9070937; DOI=10.1006/geno.1996.4544;
 RA Liao F., Lee H.-H., Farber J.M.,
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled
 RT receptor related to chemokine receptors and located on chromosome
 RT 6q27.";
 RL Genomics 40:175-180(1997).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Warren C.N., Aronstam R.S., Sharma S.V.,
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
 RA Winkling L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Alencough R.,
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
 RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
 RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
 RA Burford D.C., Burrill W., Burton J., Carter C., Carter N.P.,
 RA Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
 RA Collier R.E., Collins J.B., Colman L.R., Corby R.N., Coville G.J.,
 RA Culley K.M., Dhali P., Davies J., Dunn M., Earthworm M.E.,
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
 RA Frankland J., French L., Garner P., Garnett U., Ghori M.J.,
 RA Gilly L.M., Gillson C.J., Gilchrist R.J., Graham D.V., Grant M.,
 RA Griddle S., Griffiths C., Griffiths M.N.D., Hall R., Hall K.S.,
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
 RA Humphrey S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Leverhulme M., Lloyd C.R., Lloyd D.M.,
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLeay K.,
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
 RA Novik K.L., Oliver K., Overton-Latty E.K., Parker A., Patel R.,
 RA Pearce A.V., Peck A.I., Phillips B.J.C.T., Phillips P., Plumb R.W.,
 RA Porter K.M., Ramsey Y., Raby S.A., Rice C.M., Rose M.T., Searle S.M.,

RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
 RA Squares S.L., Stewart C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromas A., Tubby B.,
 RA Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
 RA Whitaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
 RA Durbin R., Hubbard T., Suleiron J.E., Dunham I., Rogers J., Beck S.,
 RT "The DNA sequence and analysis of human chromosome 6.";
 RL Nature 425:805-811(2003).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Pancreas;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buerow K.H., Scheef C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3
 CC alpha/LARC and subsequently transduces a signal by increasing the
 CC intracellular calcium ions level.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Spleen, lymph nodes, appendix, and fetal
 CC liver. Expressed in lymphocytes, T cells and B cells but not in
 CC natural killer cells, monocytes or granulocytes.
 CC -1- INDUCTION: By interleukin-2.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-6 is the initiator.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL contribution -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U45984; AAB62714.1; -;
 DR EMBL: Z79784; CAB02144.1; ALT_INIT.
 DR EMBL: U60000; AAB06949.1; -;
 DR EMBL: U68030; AAC51124.1; -;
 DR EMBL: U68032; AAC51125.1; -;
 DR EMBL: AY242126; CAB99328.1; -;
 DR EMBL: AL121935; CAB99328.1; -;
 DR EMBL: BC037960; AAH37960.1; -;
 DR HSSP: P34956; 1DD0.
 DR Genew: HGNC:1607; CCR6.
 DR MIM: 601835; -;
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0004950; F: chemokine receptor activity; TAS.
 DR GO: GO:0004872; F: receptor activity; TAS.
 DR GO: GO:0019735; P: antimicrobial humoral response (sensu Verte. .); TAS.
 DR GO: GO:0006928; P: cellular humoral response (sensu Verte. .); TAS.
 DR GO: GO:0006968; P: cellular defense response; TAS.
 DR GO: GO:0006935; P: chemotaxis; TAS.
 DR GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
 DR GO: GO:0006959; P: humoral immune response; TAS.
 DR GO: GO:0007165; P: signal transduction; TAS.

